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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:27:29 ; Search time 21.0526 Seconds
(without alignments)

1828.118 Million cell updates/sec

Title: US-10-797-248A-3

Perfect score: 2086

Sequence: 1 MAARNCTKALRPLRQLATP.....IRNLIEIWAGRSLRPENQK 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR 80.1*

1: PIR1;*

2: PIR2;*

3: PIR3;*

4: PIR4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2086	100.0	400	1 JC1428	ketol-acid reducto
2	1508	72.3	395	1 A24709	ketol-acid reducto
3	1494.5	71.6	404	2 T40532	ketol-acid reducto
4	497	23.8	333	2 F70407	aceohydroxy acid
5	486	23.3	332	2 H75044	ketol-acid reducto
6	484.5	23.2	331	2 AC1694	ketol-acid reducto
7	483	23.2	342	2 C69644	ketol-acid reducto
8	480.5	23.0	331	2 AB1323	ketol-acid reducto
9	469.5	22.5	581	2 T06825	ketol-acid reducto
10	465	22.3	591	1 S30145	ketol-acid reducto
11	456	22.3	591	2 T45681	ketol-acid reducto
12	463	22.2	335	2 C90204	ketol-acid reducto
13	463	22.2	337	2 A96911	ketol-acid reducto
14	459.5	22.0	340	2 C84032	ketol-acid reducto
15	458.5	22.0	336	2 D72362	ketol-acid reducto
16	456	21.9	331	2 AD2095	ketol-acid reducto
17	450	21.6	348	1 F64492	ketol-acid reducto
18	444	21.3	367	1 A47031	ketol-acid reducto
19	442.5	21.2	334	2 F89997	alpha-keto-beta-hy
20	438.5	21.0	595	1 S17180	ketol-acid reducto
21	432.5	20.7	336	2 G95051	ketol-acid reducto
22	432.5	20.7	340	2 C97922	ketol-acid reducto
23	429	20.6	363	2 C75387	ketol-acid reducto
24	427.5	20.5	337	2 C81801	ketol-acid reducto
25	427.5	20.5	337	2 F81066	ketol-acid reducto
26	415	19.9	340	2 B66778	ketol-acid reducto
27	414.5	19.9	332	2 H69497	probable ketol-aci
28	409	19.6	344	1 S35140	ketol-acid reducto
29	405.5	19.4	333	2 A69059	ketol-acid reducto

ALIGNMENTS

RESULT 1

JC1428
ketol-acid reductoisomerase (EC 1.1.1.86) - Neurospora crassa
N;Alternate names: alpha-keto-beta-hydroxyacyl reductoisomerase
C;Species: Neurospora crassa
C;Date: 10-Sep-1999 #sequence_change 05-Oct-2004
C;Accession: JC1428
R;Sista-H-r-Bowman, B.
(Gene 120, 115-116, 1992)
A;Title: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-be
A;Reference number: JC1428; PMID:93013010; PMID:1398116
A;Accession: JC1428
A;Molecule type: DNA
A;Introns: 68/1; 78/3; 170/3; 392/3
C;Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase homology <KAR>
C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase
F;87-273/Domain: ketol-acid reductoisomerase homology

Query Match 100.0%; Score 2086; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 6.9e-146;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAARNCTKALRPLRQLATPAVORRTFVAAASAVRASVAKAAAPARQQVRCVTKMTDFA 60
Db 1 MAARNCTKALRPLRQLATPAVORRTFVAAASAVRASVAKAAAPARQQVRCVTKMTDFA 60
Qy 1 MAARNCTKALRPLRQLATPAVORRTFVAAASAVRASVAKAAAPARQQVRCVTKMTDFA 60
Db 1 MAARNCTKALRPLRQLATPAVORRTFVAAASAVRASVAKAAAPARQQVRCVTKMTDFA 60
Qy 61 GHKEBEVHERADWPAEKKLIDYFKNDTLALIGYGSQGHGQGLNLNRDNGLNVIVGVRKGKSW 120
Db 61 GHKEBEVHERADWPAEKKLIDYFKNDTLALIGYGSQGHGQGLNLNRDNGLNVIVGVRKGKSW 120
Qy 121 EDIQDGWPGKGLFQDVEAISRGTTIWNLLSDAQ2ETBWHPKPQTTKGKTLYFSGHFS 180
Db 121 EDIQDGWPGKGLFQDVEAISRGTTIWNLLSDAQ2ETBWHPKPQTTKGKTLYFSGHFS 180
Qy 181 PVEFKDLTKVEPTDVTDVILVAPKGSGRTVSLFREGRINSSFAYVQDVTGKAKVAL 240
Db 181 PVEFKDLTKVEPTDVTDVILVAPKGSGRTVSLFREGRINSSFAYVQDVTGKAKVAL 240
Qy 241 GVAVGSGLYETTFFKEVSDLYGRRGCLMGGIHGMPLAQEVLRERGHSPSEAFNTVE 300
Db 241 GVAVGSGLYETTFFKEVSDLYGRRGCLMGGIHGMPLAQEVLRERGHSPSEAFNTVE 300
Qy 301 BATQSLPLIGAHMDMMFDASTTARGIDWTPKFDKDALPKVPNLYDSVKNGDRK 360
Db 301 BATQSLPLIGAHMDMMFDASTTARGIDWTPKFDKDALPKVPNLYDSVKNGDRK 360
Qy 361 SLEYNQSDYRERYEAEDETRNLIEWRACKRSLRPENQK 400

Db	361	SLEFNQPDYERYEAELDIBRNLEIWRAGRSLSRPENQ 400	C;Accession: T40532; T43303; T42540 A;Submitted to the EMBL Data Library, May 1998 A;Reference number: 221935
RESULT 2			
A2	4109	ketol-acid reductoisomerase (EC 1.1.1.86) ILV5 - yeast (Saccharomyces cerevisiae)	C;Accession: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
N;Alternate names: acehydroxyacid reductoisomerase ILV5; protein YLR3	C;Species: <i>Saccharomyces cerevisiae</i>	C;Accession: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004	C;Accession: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
R;Petersen, J.G.L.; Holmberg, S.	R;Accession: A24709; PMID: 851463	R;Accession: A24709; PMID: 851463	R;Accession: A24709; PMID: 851463
Nucleic Acids Res. 14, 9631-9651. 1986	A;Title: The ILV5 gene of <i>Saccharomyces cerevisiae</i> is highly expressed.	A;Title: The ILV5 gene of <i>Saccharomyces cerevisiae</i> is highly expressed.	A;Title: The ILV5 gene of <i>Saccharomyces cerevisiae</i> is highly expressed.
A;Cross-references: UNIPROT:P06168; UNIPARC:UPI000012D529; EMBL:X04969; NID:93826; PIDN:R,Du, Z.	A;Cross-references: UNIPROT:P06168; UNIPARC:UPI000012D529; EMBL:X04969; NID:93826; PIDN:R,Du, Z.	A;Cross-references: UNIPROT:P06168; UNIPARC:UPI000012D529; EMBL:X04969; NID:93826; PIDN:R,Du, Z.	A;Cross-references: UNIPROT:P06168; UNIPARC:UPI000012D529; EMBL:X04969; NID:93826; PIDN:R,Du, Z.
A;Description: The sequence of <i>S. cerevisiae</i> cosmid 9638.	A;Description: The sequence of <i>S. cerevisiae</i> cosmid 9638.	A;Description: The sequence of <i>S. cerevisiae</i> cosmid 9638.	A;Description: The sequence of <i>S. cerevisiae</i> cosmid 9638.
A;Accession: S51459	A;Accession: S51459	A;Accession: S51459	A;Accession: S51459
A;Residues: 1-395 <D2Z>	A;Residues: 1-395 <D2Z>	A;Residues: 1-395 <D2Z>	A;Residues: 1-395 <D2Z>
A;Cross-references: UNIPARC:UPI000012D529; EMBL:U19102; NID:9609396; PIDN:AB67753.1; PI	A;Cross-references: UNIPARC:UPI000012D529; EMBL:U19102; NID:9609396; PIDN:AB67753.1; PI	A;Cross-references: UNIPARC:UPI000012D529; EMBL:U19102; NID:9609396; PIDN:AB67753.1; PI	A;Cross-references: UNIPARC:UPI000012D529; EMBL:U19102; NID:9609396; PIDN:AB67753.1; PI
A;Genetics: SGD:ILV5; MIPS:YLR355C	A;Genetics: SGD:ILV5; MIPS:YLR355C	A;Genetics: SGD:ILV5; MIPS:YLR355C	A;Genetics: SGD:ILV5; MIPS:YLR355C
A;MAP position: 12R	A;MAP position: 12R	A;MAP position: 12R	A;MAP position: 12R
C;Superfamily: ketol-acid reductoisomerase; fungal type; ketol-acid reductoisomerase homolog	C;Superfamily: ketol-acid reductoisomerase; fungal type; ketol-acid reductoisomerase homolog	C;Superfamily: ketol-acid reductoisomerase; fungal type; ketol-acid reductoisomerase homolog	C;Superfamily: ketol-acid reductoisomerase; fungal type; ketol-acid reductoisomerase homolog
C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrial; oxidoreductase	C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrial; oxidoreductase	C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrial; oxidoreductase	C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrial; oxidoreductase
F;P1-267/Domain: ketol-acid reductoisomerase homolog <KAR>	F;P1-267/Domain: ketol-acid reductoisomerase homolog <KAR>	F;P1-267/Domain: ketol-acid reductoisomerase homolog <KAR>	F;P1-267/Domain: ketol-acid reductoisomerase homolog <KAR>
Query Match	7 TKAQLPLRQLATPAVORTFVAASAVRASTAVKAVAAAPARQ----RGVKTMDA 60	Query Match	7 TKAQLPLRQLATPAVORTFVAASAVRASTAVKAVAAAPARQ----RGVKTMDA 60
Best Local Similarity	72.3%	Score	Score 1508.5; DB 1; Length 395;
Matches	295; Conservative 39; Mismatches 50; Indels 17; Gaps 5;	Matches	295; Conservative 39; Mismatches 50; Indels 17; Gaps 5;
Qy	7 TKAQLPLRQLATPAVORTFVAASAVRASTAVKAVAAAPARQ----RGVKTMDA 60	Qy	7 TKAQLPLRQLATPAVORTFVAASAVRASTAVKAVAAAPARQ----RGVKTMDA 60
Db	4 TQAARLICNSRVTAA--KRTF---ALATRAA---AVSRPAARFVKEPMITRGLKQINFQ 54	Db	4 TQAARLICNSRVTAA--KRTF---ALATRAA---AVSRPAARFVKEPMITRGLKQINFQ 54
Qy	61 GHKEEVHERADWPAEKLIDYFKNDTFLALIGYSQSGHQLGNNLIRDNGLAVIYGVRKQKSW 120	Qy	61 GHKEEVHERADWPAEKLIDYFKNDTFLALIGYSQSGHQLGNNLIRDNGLAVIYGVRKQKSW 120
Db	55 GTIVETVYERADWREKFLDQGPKNLFDVDBAISGTTIYNNLLSDAQSETWPPIKQPTIKGKTYFSGF 180	Db	55 GTIVETVYERADWREKFLDQGPKNLFDVDBAISGTTIYNNLLSDAQSETWPPIKQPTIKGKTYFSGF 180
Qy	121 EDI1QDGWPGKNNFDVTPDVLVAPKGSGRTYRSLSFREGRGSINSFAYVDTGKAEKVAL 240	Qy	121 EDI1QDGWPGKNNFDVTPDVLVAPKGSGRTYRSLSFREGRGSINSFAYVDTGKAEKVAL 240
Db	115 KAA1EDGWPVPGKNNLPTVEDAIKRGSSYNNLLSDAQSETWPPIKQPTIKGKTYFSGF 174	Db	115 KAA1EDGWPVPGKNNLPTVEDAIKRGSSYNNLLSDAQSETWPPIKQPTIKGKTYFSGF 174
Qy	181 PVFKDLTKEVTPDVLVAPKGSGRTYRSLSFREGRGSINSFAYVDTGKAEKVAL 240	Qy	181 PVFKDLTKEVTPDVLVAPKGSGRTYRSLSFREGRGSINSFAYVDTGKAEKVAL 240
Db	175 PVFKDLTKEVTPDVLVAPKGSGRTYRSLSFREGRGSINSFAYVDTGKAEKVAL 234	Db	175 PVFKDLTKEVTPDVLVAPKGSGRTYRSLSFREGRGSINSFAYVDTGKAEKVAL 234
Qy	241 GVAVSGSYVLYETTFKEVSYSDLYGERGLMGCGTHGMPLAQEVYLREGRHSSEAFNETV 300	Qy	241 GVAVSGSYVLYETTFKEVSYSDLYGERGLMGCGTHGMPLAQEVYLREGRHSSEAFNETV 300
Db	235 AVAIGSGTVYQTFERETNSDLYGERGLMGCGTHGMPLAQEVYLREGRHSSEAFNETV 294	Db	235 AVAIGSGTVYQTFERETNSDLYGERGLMGCGTHGMPLAQEVYLREGRHSSEAFNETV 294
Qy	301 EATQSLYPLIGAHGMDMNFACSTTARGAIWTPKPDALKPVPNNLYDSVYNGDGRK 360	Qy	301 EATQSLYPLIGAHGMDMNFACSTTARGAIWTPKPDALKPVPNNLYDSVYNGDGRK 360
Db	295 EATQSLYPLIGKGYMDMNYDACSSTTARGALDMPYKPNALKPVPQDLYESTKNGTETR 354	Db	295 EATQSLYPLIGKGYMDMNYDACSSTTARGALDMPYKPNALKPVPQDLYESTKNGTETR 354
Qy	361 SLEFNQPDYERYEAELDIBRNLEIWRAGK--RSURPENO 399	Qy	361 SLEFNQPDYERYEAELDIBRNLEIWRAGK--RSURPENO 399
Db	355 SLEFNQPDYERYEAELDIBRNLEIWRAGK--RSURPENO 395	Db	355 SLEFNQPDYERYEAELDIBRNLEIWRAGK--RSURPENO 395
RESULT 3			
T40532	ketol-acid reductoisomerase (EC 1.1.1.86) [similarity] - fission yeast (Schizosaccharomyces pombe)	T40532	ketol-acid reductoisomerase (EC 1.1.1.86) [similarity] - fission yeast (Schizosaccharomyces pombe)
C;Species: <i>Schizosaccharomyces pombe</i>	C;Species: <i>Schizosaccharomyces pombe</i>	C;Species: <i>Schizosaccharomyces pombe</i>	C;Species: <i>Schizosaccharomyces pombe</i>
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004	Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004	Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004	Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004

acetohydroxy acid isomero reductase - Aquifex aeolicus	Qy	75 EKLIDYFKNDTLLALIGYGSQGHGGGLNRLDNGLNIVGVRKNGKSWEDAIDQGWVPGKNL 134		
C;Species: Aquifex aeolicus	Db	12 EVNDILKDKTIVAVTGYGNGQEAQAKNRDGSVHILGRPSGSWKZRAEKDGF---EV 67		
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004	Qy	135 FDVDEAISRGTTVNLILSDAQSETWPH-PIKPOITKGKTYLFSHGSFSPVFDLTKYEVET 193		
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Or	Db	68 YTTEAVKADIVHILIPVQPKVYHIEPIVREGQALGFSGHNFNTHYKQ1VP--PE 124		
V;Nature 392, 353-358, 1998	Qy	194 DWDYLVAPKSGSRTVSLFREGRGINSFAYQDTGKAKERAVALGTVAVG---SGVLY 250		
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.	Db	125 YWDYLVAPKSPGKVRKYLEGGVPAVATQDYNAGDALAMAKAIGTRAVGI- 183		
A;Reference: PMID:537320	Qy	251 ETTPEKEYSDLIGERGCLMGGIHMFLAQYEYLRERGHSPSAFAFNTEVBEATOSLYPLI 310		
A;Accession: PMID:537320	Db	184 ETTPEKEYSDLIGERGCLMGGIHMFLAQYEYLRERGHSPSAFAFNTEVBEATOSLYPLI 242		
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	Qy	311 GAHGMDDWMDACSTTARRGAIDWTPK-FKDALKPWNFLYDSVYKNGDDEKRSLEYNSQPD 369		
A;Molecule type: DNA	Db	243 YERFTGMLKAVSDTAKYGLTVGPVTDHYKEMMKFAERVYSGEFAK--EWISRAD 299		
A;Residues: 1-33 <AQP>	Qy	370 -YRERYEABDSDTRNLNEIWRAGK 391		
A;Cross-references: UNIPROT:067289; UNIPARC:UPI0000056582; GB:AE000730; NID:92983674; PI	Db	300 KASEVYELMLKPIEEHEIEKVGR 322		
P;21/203/Domain: ketol-acid reductoisomerase	Db	RESULT 6		
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase not shown; archaea/bacteria homology <KAR>	Db	AC1694 ketol-acid reductoisomerase (acetohydroxy-acid isomero reductase) homolog ilvc [Imported]		
P;21/203/Domain: ketol-acid reductoisomerase	Qy	C;Species: Listeria innocua		
Matches 115; Conservative 70; Mismatches 124; Indels 22; Gaps 9;	Db	C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004		
Qy	78 LDYFKNDTLLALIGYGSQGHGGGLNRLDNGLNIVGVRKNGKSWEDAIDQGWVPGKNLFPV 137	C;Accession: AC1694		
Db	122 LDILDKVIALIGYGSQGHHALNRLDSGIVNLGHESRSRERAKAEGF---EVYTP 67	R;Glaeser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Domangue-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.J. Jones, L.M.; Karst, U.		
Query Match Score 23.8%; Best Local Similarity 34.7%; Pred. No. 4.6e-124	Qy	Science 294, 849-852, 2001		
Matches 115; Conservative 70; Mismatches 124; Indels 22; Gaps 9;	Db	A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madiueno, E.; Maitournam, A.; Mat		
Qy	78 LDYFKNDTLLALIGYGSQGHGGGLNRLDNGLNIVGVRKNGKSWEDAIDQGWVPGKNLFPV 137	ok, C.; Schlueter, T.; Simeos, N.; Tierre, J.A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of <i>Listeria</i> species.		
Db	122 LDILDKVIALIGYGSQGHHALNRLDSGIVNLGHESRSRERAKAEGF---EVYTP 67	A;Reference number: AB1077; PMID:21537279; PMID:11679669		
Query Match Score 23.8%; Best Local Similarity 34.7%; Pred. No. 4.6e-124	Db	A;Accession: AC1694		
Matches 115; Conservative 70; Mismatches 124; Indels 22; Gaps 9;	Qy	A;Status: preliminary		
Qy	138 DEASIRGTIVNLILSDAQSETWPH-PIKPOITKGKTYLFSHGSFSPVFDLTKYEVET 196	A;Molecule type: DNA		
Db	68 REAAKADILMFILPDTQPEVYNEVEPLNSKTLAPAHGENTHFRQ1VP---PKD0 124	A;Cross-references: UNIPARC:UPI000005759; GB:AL592022; PID: CAC97323.1; PID:g16414607; C		
Qy	197 VLYVAPKGSGRTVSLFREGRGINSFAYQDTGKAKERAVALGVAVGS--GVLXTTP 254	C;Generic: ilvc		
Db	125 VFMVAPKGPSGHVLVRMNTYSEKQVPAVTHQDASCTKQKALAYAKGTCATRAGVETP 184	C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase		
Qy	197 VLYVAPKGSGRTVSLFREGRGINSFAYQDTGKAKERAVALGVAVGS--GVLXTTP 254	Query Match Score 23.2%; Best Local Similarity 38.2%; Pred. No. 3.8e-28; Length 331;		
Db	125 VFMVAPKGPSGHVLVRMNTYSEKQVPAVTHQDASCTKQKALAYAKGTCATRAGVETP 184	Best Local Similarity 38.2%; Pred. No. 3.8e-28; Length 331;		
Qy	255 EKEVTSPLIGERGCLMGGIHMFLAQYEYLRERGHSPSAFAFNTEVBEATOSLYPLI 314	Mismatches 50; Conservative 50; Mismatches 117; Indels 35; Gap 10;		
Db	185 KEETEDPLFSEQMVULGGTATLAKGFTLVNAGYQPEVAYFECLE-LKLIVDLYEHG 243	Db	Qy	79 DYFKNDTLLALIGYGSQGHGGGLNRLDNGLNIVGVRKNGKSWEDAIDQGWVPGKNL 133
Qy	315 MDWMDACSTTARRGAIDWTPKFDALKPWNFLYDSVNGDERKRSLEYN--SQPDY-- 370	8 DAYKONNALEGKTVAVTGYGSQGHASHQNLDRNGNNVIGIRE GKAESARNDGF---D 62		
Db	244 ISGMYRISIISDTAKYGDVTGRERITYKVKPMEKTLLEIIGKGEFAREWILENKAGRPTVYA 303	Db	Qy	134 LFDVDEAISRGTTVNLILSDAQSETWPH-PIKPOITKGKTYLFSHGSFSPVFDLTKYEVET 192
Qy	371 ---RER---YEAELEDEIRNLIEIWRAGKRSLR 395	63 VTSVSEALEKADIVMILIPDEQETYENETKPNLKGNALYFARGFNTHF---DVINPP 119		
Db	304 LLERDREHHLVKEVGBELRKMPW-LGKCHLK 333	Db	Qy	193 TWDYLVAPKSGSRTVSLFREGRGINSFAYQDTGKAKERAVALGVAVGS--GVLXTTP 250
RESULT 5	Db	120 SDYDVFVLYAPKGPSGHVTRTFVEGGAVPSLFLAYQDTGKAKERAVALGVAVGS--GVLXTTP 179		
H75044 ketol-acid reductoisomerase (ilvc)	Qy	251 ETTPEKEYSDLIGERGCLMGGIHMFLAQYEYLRERGHSPSAFAFNTEVBEATOSLYPLI 310		
C;Species: Pyrococcus abyssi	Db	180 ETTPEKEYSDLIGERGCLMGGIHMFLAQYEYLRERGHSPSAFAFNTEVBEATOSLYPLI 238		
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004	Qy	311 GAHGMDDWMDACSTTARRGAIDW-----TPKFDALKPWNFLYDSVNGDERKRSLEYN--YDSVTKN 354		
R;Anonymous, Genoscope	Db	239 YEGGMKMRHSISNTAEXY--DVSGSPRVVATDKRAMKEVLTIDQNGNEAKSFIDDNK 296		
A;Submitted to the EMBL Data library, July 1999	Qy	A;Cross-references: UNIPROT:09UZ09; UNIPARC:UPI000003453B; GB:AU248287; GB:NID:AU096836; NID:AU:Experimental source: strain Orsay		
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure	Db	A;Accession: H75044		
A;Reference number: A75001	Qy	A;Status: preliminary		
A;Molecule type: DNA	Db	A;Cross-references: UNIPROT:09UZ09; UNIPARC:UPI000003453B; GB:AU248287; GB:NID:AU096836; NID:AU:Experimental source: strain Orsay		
A;Residues: 1-332 <KAW>	Db	A;Accession: H75044		
A;Cross-references: UNIPROT:09UZ09; UNIPARC:UPI000003453B; GB:AU248287; GB:NID:AU096836; NID:AU:Experimental source: strain Orsay	Qy	A;Gene: ilvc; PAB0889		
A;Genetics:	Db	C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase		
A;Residues: 1-332 <KAW>	Qy	F;24-206/Domain: ketol-acid reductoisomerase homology <KAR>		
A;Cross-references: UNIPROT:09UZ09; UNIPARC:UPI000003453B; GB:AU248287; GB:NID:AU096836; NID:AU:Experimental source: strain Orsay	Db	Best Local Similarity 37.8%; Pred. No. 3e-28; Mismatches 63; Conservative 122; Mismatches 122; Mismatches 63; Conservative 70; Mismatches 124; Indels 18; Gaps 9;		

Qy	1	MAA---RNCYKALPRLAROLATP-----	-AVORTFVAAASAVASVAV 4.0
Db	1	MAAVTSSCSPAIASSKTLAKPVAASAPFTNLSEKSLSPQSIARRSITVGSALGAT---	57
Qy	41	KAAVAPPAQRQYRGVXTMDF-----	-AGKKEEYHERADWPAEKLLDFFKDN---DTLA 8.7
Db	58	KVSSAPPATHEV---SLDFTTSVFKKERVNLAGEYEIVRGGLDFLPHLPDAFKGKIQG 11.3	
Qy	88	LIGGSQGHGQGLNIRD-----	-NGLNVLYVGKKGKSMEDAQDGWYPGK-NLFDVDEA 14.0
Db	114	VIGWSQGPQAQNDRSLVEAKSDIVVKGLRGSSSNEARAGFSEKCTLGDIWET 17.3	
Qy	141	ISRGITIVMILLSDAQPSETWPHIKPQITKGKTLFYSHGSPSPVPKDLTKEVPPDVIVLV 200	
Db	174	ISGSIVLVLISDSDQADNVEYKIFSHLKENSLIGLHSFLGHLSQIGLDFPKNFSIVAV 23.3	
Qy	201	APKGSGRTYRSLFRGR-----	-GINSSPAVYQDVTGKAKEKAVALGVAVGSGSYLYETTFFE 255
Db	234	CPKGKGPSPVRLYQGKEINGAGINSSFGVHQDVGRATNVALGWSVALGSPPFTTLE 293	
Qy	256	KEVSDLYGERGLMGGTH-----	
Db	294	QEYKSDIFGERGLIGAVHGIVESLFRRTYKAYASFYPCMELYECYDVAVGSEI1RSVVLAGRFFYKEGLP 413	
Qy	276	-----	275
Db	354	LAVYNALSEDGKKEFKEKAYSFPCMELYECYDVAVGSEI1RSVVLAGRFFYKEGLP 413	
Qy	276	-----	275
Db	414	AFPNGKIDQTRMVKGERVTRSPAGDGPGLYPTFAGFEVAMMATEVLRKGHSEYI 473	
Qy	295	FNETYVEATOSLYPLIGAHGMDMFDACSTTARGADWTPKF 337	
Db	474	INESTVSDLSNPFMHARGVSFMVDNCSTTARLGSRKWAPF 516	
RESULT 10			
S30145	ketol-acid reductoisomerase (EC 1.1.1.86) precursor - <i>Arabidopsis thaliana</i>		
N	Alternative names: acetohydroxy acid isomero-reductase		
C	Species: <i>Arabidopsis thaliana</i> (mouse-eared cress)		
C	Date: 10-sep-1999 #sequence revision 10-Sep-1999 #text_change 05-Oct-2004		
C	Accession: S30145; S34040; S36884		
R	Curien, G.; Dumas, R.; Douce, R.		
R	Plant Mol. Biol. 21, 717-722, 1993		
A	Title: Nucleotide sequence and characterization of a cDNA encoding the acetohydroxy acid isomero-reductase from <i>Arabidopsis thaliana</i> (mouse-eared cress).		
A	Accession: S30145; MUID:93192533; PMID:8418371		
A	Molecule type: mRNA		
A	Residues: 1-591 <CUT>		
A	Cross-references: UNIPROT:Q05758; UNIPARC:UP10000171F83; EMBL:X68150		
R	Submitted to the EMBL Data Library, July 1992		
A	Reference number: S30140		
A	Molecule type: mRNA		
A	Residues: 1-284; R: 286-591 <DOM>		
A	Cross references: UNIPARC:UPI000016DB7B; EMBL:X68150; NID:9288062; PIDN:CAA482		
R	Dumas, R.; Curien, G.; Dumas, R.; Douce, R.		
R	Biochem. J. 294, 821-828, 1993		
A	Title: Branched-chain-amino-acid biosynthesis in plants: molecular cloning and expression of a cDNA encoding the acetohydroxy acid isomero-reductase from <i>Arabidopsis thaliana</i> (mouse-eared cress).		
A	Accession number: S36884; MUID:93393563; PMID:8379936		
A	Molecule type: DNA		
A	Residues: 1-578, 'A', 580-591 <DU2>		
C	Cross references: UNIPARC:UPI0000000A7B; EMBL:X659880; NID:9402551; PIDN:CAA495		
A	Genome: nuclear		
A	Introns: 99/3; 13/0/3; 152/3; 199/3; 275/3; 315/1; 361/3; 417/3; 469/3		
C	Superfamily: ketosterol; isoleucine-valine biosynthetic pathway; plant type; ketosterol-acid reductoisomerase; plant type; isomerase; oxidoreductase		
C	Keywords: chloroplast; isoleucine-valine biosynthesis; isomerase; oxidoreductase		

F:1-67/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:68-591/Product: ketol-acid reductoisomerase #status predicted <MAT>
F:123-321/Domain: ketol-acid reductoisomerase homology <KAR>
Query Match Score 465; DB 1; Length 591;
Best Local Similarity 27.2%; Pred. No. 2.3e-26;
Matches 132; Conservative 68; Mismatches 128; Indels 158; Gaps 7;
Query 7 TKALPRLAROLATPAVQORTTFVAAAASVAVSAYAKKA_VAAPARQQVQVGKTMDFAGHKKE 65
Db 44 SKSLRSLT---ATVAGNGATGSSLAARVSSAVAKAPVSLDFETSVFKCEKVSLAGVVEY 100
Query 66 VHERADWPAAEKLQDFKRN-DTIALIGKGSQGSGHQGKQGKLRD-----NGLNVTVGVRKNGK 118
Db 101 IVRGGRDLFLKHLPLDAFKGKQIKOQVIGVIGCSQGPQAQNLRSILVEAKASDIVVIGLKGSR 160
Query 119 SWED1QDQGW-W-PGKNUFDVDEAISRGTTIVMNLSSDAQSETWPHIKPQITKGKTYLFSH 177
Db 161 SFEVARAAGFTERSGTLGDIWEITAGSDLVNLISDAQADNTYKFSHMKPNSIGLGLSH 220
Query 178 GFSPVVKDOLTKVKEVPTDVILVAKPSSGRYTRSLPREGR-----GINSSPRAVYQDVTGK 232
Db 221 GFLIGLHQGLSSGLDFPKNISVWAVCPKMGPSVTRLIVQGKETINGAGINASPAHVQDVGDR 280
Query 233 AKEKAVALGVAVGSSGYIYETTFKEVYSDLYGERGCCMGGHG----- 275
Db 281 AADVALGMSVALSPFATTLEQEVRSDFIGERGLLGAVGIVVSSLFRRTENGSMSBD 340
Query 276 ----- 275
Db 341 LAYKNTVECITGTISRTISTQMLAVYNSLSEGRKDFETAYSASTYPCMBILYECYEDV 400
Query 276 ----- 275
Db 401 QSGSEIRSVVLAGRRFYKEKGLPAFPMGNIIDOTRMVKGERVRKSRRPAGDLGPLYPTAG 460
Query 276 ---MFLLQYEVTLERGHSPSEAFNFTVEETATQSLYPLIGAHGMDMFDACSTTARGA 331
Db 461 VYVALMMQAIIELKCHSYSSBLLINNEVIESYDLMNPFMARGVSSFMVDNCSTTARGLGSR 520
Query 332 DWTTPKF 337
Db 521 KWAPRF 526
RESULT 11
T45681
ketol-acid reductoisomerase - <i>Arabidopsis thaliana</i>
N-Alternative names: protein FlAP22.200
C-Species: <i>Arabidopsis thaliana</i> (mouse-ear cress)
C-Accession: T45681
R.D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lem
Submitted to the Protein Sequence Database, January 2000
A-Reference number: 223011
A-Accession: T45681
A-Status: preliminary
A-Molecule type: DNA
A-Residues: 1-591 <DAN>
A-Cross-references: UNIPROT:Q05758; UNIPARC:UPI000000007B; EMBL:AL137082
C-Genetics:
A-MP position: 3
A-Introns: 99/3; 130/3; 152/3; 199/3; 275/3; 315/1; 361/3; 417/3; 469/3
A-Note: FlAP22.200
C-Superfamily: ketol-acid reductoisomerase, plant type; ketol-acid reductoisomerase
F:123-321/Domain: ketol-acid reductoisomerase homology <KAR>
Query Match Score 465; DB 2; Length 591;
Best Local Similarity 27.2%; Pred. No. 2.3e-26;
Matches 132; Conservative 68; Mismatches 128; Indels 158; Gaps 7;
Query 7 TKALPRLAROLATPAVQORTTFVAAAASVAVSAYAKKA_VAAPARQQVQVGKTMDFAGHKKE 65

Query Match 22.0%; Score 459.5; DB 2; Length 340;
 Best Local Similarity 39.3%; Pred. No. 2.7e-26;
 Matches 107; Conservative 52; Mismatches 96; Indels 17; Gaps 7;

Qy 85 TLALIGGGGSGCHGQGINLNRLQNLNTVYGRKNGKSWEDALODGWVPGKRNLFVDDEAISRG 144
 Db 19 TVAIIGGGSGCHGQGINLNRLQNLNTVYGRKNGKSWEDALODGWVPGKRNLFVDDEAISRG 144
 Qy 145 TIVMQLLSDAAQSETWPH- IKPQITKKGTLVYGRKNGKSWEDALODGWVPGKRNLFVDDEAISRG 144
 Db 74 DVIMILLPDEHOPTVYKNEPELSEGKTLAPAHGENVHQIWP---PATDVFLAANK 130
 Qy 204 GSGRTVRSLSPREGRGINSNSPAXYQDVTGKAKRKAVALGAVGSGY--LYETTFFKEVYSD 261
 Db 131 GPGHLVRRTIVDAGVPGVLYAVYQDTPGQARDIALAYSRSKNGSARAGVETTFOBETED 190
 Qy 262 LYGERGGCLMGIGHGMFLAYEVLTGKAKRKAVALGAVGSGY--LYETTFFKEVYSD 261
 Db 191 LFGEQAVLCCGTSALVYKAGFETLVEAGYQEVAVFPECLHE-LKLIVDLYMEGGLLEVMRYS 249
 Qy 322 CSTTARRGAIDWTPKF---KDALKRPVFNLL 348
 Db 250 ISDTAQWGDFOAGPRVVTAAETKQAMKDIISDI 281

RESULT 15

D72362
 ketol-acid reductoisomerase - *Thermotoga maritima* (strain MSB8)
 C;Species: *Thermotoga maritima*
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004
 C;Accession: D72362
 R;: Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haff, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A;Reference number: A72200; MUID:99287316; PMID:10360571
 A;Accession: D72362
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-336 <ARN>
 A;Cross-references: UNIPROT:Q9WZ20; UNIPARC:UPI000012D560; GB:AE000512; NID
 A;Experimental source: strain MSB8
 A;Gene: TM0550
 C;Superfamily: ketol-acid reductoisomerase; archaea/bacteria type; ketol-acid reductoisomerase
 P;21-203/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 22.0%; Score 458.5; DB 2; Length 336;
 Best Local Similarity 37.9%; Pred. No. 3.2e-26;
 Matches 106; Conservative 57; Mismatches 104; Indels 13; Gaps 6;

Qy 78 LDYFKNDTIALIGGGSGCHGQGINLNRLQNLNTVYGRKNGKSWEDALODGWVPGKRNLFVD 137
 Db 12 LNLTKDKKAIGGSGCHGQGINLNRLQNLNTVYGRKNGKSWEDALODGWVPGKRNLFVD 137
 Qy 138 DEASRGTTIWNLLSDAAQSETWPHIKPQITKKGTLVYGRKNGKSWEDALODGWVPGKRNLFVD 196
 Db 68 EEAAKEADLIMILLPDEHOPTVYKNEPELSEGKTLAPAHGENVHQIWP---PATDVFLAANK 124
 Qy 197 VILVAPKGSSGRTVRSLSFREGGRINNSFAYQDVTGKAKRKAVAL--GVAVGSGYLYETTF 254
 Db 125 VTMIAPKSSPHIIVREYVEGRGVPAVVAQDTGKAKDIALAYAKGGTRAVIETTF 184

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:27:29 ; Search time 20:7895 Seconds

Sequence: (without alignments) 1828.118 Million cell updates/sec

Title: US-10-797-248a-2

Perfect score: 2071

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

203416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 203416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.4

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

30	385	18.6	340	2	G81411	ketol-acid reducto
31	372.5	18.0	344	1	S3540	probable ketol-acid
32	332	17.8	332	2	A2824	acetolactate synth
33	365	17.6	338	2	D97602	ketol-acid reducto
34	359.5	17.4	338	1	I5ECKR	ketol-acid reducto
35	337	17.2	333	1	C48648	ketol-acid reducto
36	352.5	17.0	339	2	AB3330	ketol-acid reducto
37	350.5	16.9	339	2	D97602	ketol-acid reducto
38	350.5	16.9	339	2	I5ECKR	hypothetical prote
39	339	16.4	491	1		ketol-acid reducto
40	339	16.4	491	2	D91217	ketol-acid reducto
41	41	16.4	491	2	E86053	ketol-acid reducto
42	336	16.2	333	2	D70855	probable ilvc prot
43	336	16.2	333	2	H87120	ketol-acid reducto
44	44	16.2	343	2	T45415	ketol-acid reducto
45	335	16.2	492	2	AG0473	ketol-acid reducto

ALIGNMENTS

RESULT 1
A24709
ketol-acid reductoisomerase (EC 1.1.1.86) ILV5 - Yeast (Saccharomyces cerevisiae)
N;Alternate names: acetylhydroxyacid reductoisomerase ILV5; protein L9638.7; protein YLR35C
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A24709; S51463
R;Petersen, J.G.L.; Holmberg, S.

[Nucleic Acids Res: 14: 9631-9651, 1986]
A;Title: The ILV5 gene of Saccharomyces cerevisiae is highly expressed.

A;Reference number: A24709; MUID:87117524; PMID:3027658

A;Molecule type: DNA

A;Residues: 1-395 <PET>

A;Cross-references: UNIPROT:P06168; UNIPARC:UP100012D529; EMBL:X04969; NID:93826; PIDN:CC

R;Du, Z.

Submitted to the EMBL Data Library, December 1994

A;Description: The sequence of S. cerevisiae cosmid 9638.

A;Reference number: S51459

A;Accession: S51463

A;Molecule type: DNA

A;Residues: 1-395 <DUV>

A;Cross-references: UNIPARC:UP100012D529; EMBL:U19102; NID:9609396; PIDN:AAB67753.1; PII

C;Genetics:

A;Gene: SGD:ILV5; MIPS:YLR55C

A;Cross-references: SGD:S0004347; MIPS:YLR35C

A;Cross Position: 12R

C;Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase homolog

C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase

F;81-267/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match

100.0%; Score 2071; DB 1; Length 395;

Best Local Similarity

100.0%; Pred. No. 1.4e-47;

Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 MLRTOAARLICNSRVITAKRTFAALTRAAAYSRAAPRFKPMITRSGKQINFGGTETV

Db

1 MLRTOAARLICNSRVITAKRTFAALTRAAAYSRAAPRFKPMITRSGKQINFGGTETV

QY

121 GWVQKNTFVEDAIKRSYVNLISDAQSETWPALKPLKGKTLFSGHSPVAKDL

QY

61 YERADWPRLKLFYKNTFALIGYSGCGYCGNLNDLGLNLTIGRKDGASWAKLIED

QY

61 YERADWPRLKLFYKNTFALIGYSGCGYCGNLNDLGLNLTIGRKDGASWAKLIED

QY

180

QY

121 GWVQKNTFVEDAIKRSYVNLISDAQSETWPALKPLKGKTLFSGHSPVAKDL

QY

121 GWVQKNTFVEDAIKRSYVNLISDAQSETWPALKPLKGKTLFSGHSPVAKDL

QY

180

QY

181 THYEPPKDVLVAPKGSGRTVRLFREGGRINNSYAVWNDVTKAKAHLAVALIGS

QY

181 THYEPPKDVLVAPKGSGRTVRLFREGGRINNSYAVWNDVTKAKAHLAVALIGS

QY

240

QY

<p

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RESULT 2
JCI428
ketol-acid reductoisomerase (EC 1.1.1.86) - Neurospora crassa
N|Alternative names: alpha-keto-beta-hydroxylacyl reductoisomerase
C|Species: Neurospora crassa
C|Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C|Accession: JCI428
R|Sista, H.; Bowman, B.
Gene 120, 115-118, 1992
A|Title: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-  
C;Reference number: JCI428; MUID:93013010; PMID:1398116
A|Accession: JCI428
A|Molecule type: DNA
A|Residues: 1-400 <SIS>
A|Cross-references: UNIPROT:P38674; UNIPARC:UP1000012D525; GB:M84189; NID:9168821; PIDN:  
C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase
F:87-273/Domain: ketol-acid reductoisomerase homology <KAR>
Query Match
Best Local Similarity 72.8%; Score 1508.5; DB 1; Length 400;
Matches 295; Conservative 39; Mismatches 50; Indels 17; Gaps 5;
Oy 4 TQARLICNSRVITA--KRTF--ALA TRA---AVSRPAARFVKEMITTHGKQINFG 54
Oy 7 TKALRPLAROLATPAVQRRTFVAASAVRASVAKAVAAPARQV-----RGVKTMDFA 60
Db 55 GTWETTVERADWREKPLDYEKNDTFAIGYSGQSQYSGCMLNRDNGLAVLIGVKGASW 114
Db 61 GHKEVHERADWPAEKBLDQYKDFTDNLALIGYSGQHGOGLNLRDNGLAVLIGVKGKSW 120
Db 115 KAALIEDGWPGKOLFTVEDAIKGSYVWNLSDAQSSTWPAIKPLLTGKLYFSSGFS 174
Db 121 EDAIQDGWPGKOLFDVDBAISRGTVINLSDAQSSTWPAIKPLLTGKLYFSSGFS 180
Db 175 PVRKDULTAVERPPKDDLIVLIVAPKGSGRTVRSLSRKEGRGINSYAVWMDUTGKAEKAQAL 234
Db 181 PVRKDULTKVEVPTDVIVLIVAPKGSGRTVRSLSRREGRGINSSFAVYQDVTKAKEKAVAL 240
Db 235 AVAIGSGYVQTFRENTSDYGERGCLMGIGHMFELAQYDVTRENGHSPSEAFNTE 294
Db 241 GVAWGGSYLVEETFEKEVSDLYGERGCLMGIGHMFELAQYDVTRENGHSPSEAFNTE 300
Db 295 EATOSLYPLIGKGMDDYMACTTARGALDWYPIFKQALKPVQFDLYESTKGNTETKR 354
Db 301 EATOSLYPLIGKGMDDYMACTTARGALDWYPIFKQALKPVQFDLYESTKGNTETKR 360
Db 355 SLEFNSQDYREKLEKELDTIRNMEIWKGKEVRLRPNQ 395
Db 361 SLEFNSQDYREKLEKELDTIRNMEIWKGKEVRLRPNQ 395

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C-PROCESSED; I-UNP; J-UNP; K-UNP; L-UNP; M-UNP; N-UNP; O-UNP; P-UNP; Q-UNP; R-UNP; S-UNP; T-UNP; U-UNP; V-UNP; W-UNP; X-UNP; Y-UNP; Z-UNP
 R. Purnelle, B.; Goffeau, A.; Wood, V.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, May 1998
 A-Reference number: 221935
 A-Accession: T40532
 A-Status: translated from GB/EMBL/DBJ
 A-Molecule type: DNA
 A-Residues: 1-404 <PUR>
 A-Cross-references: UNIPROT:P78827; UNIPARC:UPI00012D527; EMBL:AL023288; NID:95832408;
 submitted to the EMBL Data library, December 1997
 A-Description: S. pombe ILV5 homolog.
 A-Reference number: Z22407
 A-Accession: T43103
 A-Status: translated from GB/EMBL/DBJ
 A-Molecule type: mRNA
 A-Residues: 262-404 <KAW>
 A-Cross-references: UNIPARC:UPI000168765; EMBL:AB009603; NID:92696653; PIDN:BAA24000.1;
 R. Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
 DNA Res. 4, 363-369, 1997
 A-TITLE: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
 A-Reference number: 217323; MUID:98162722; PMID:9501991
 A-Accession: T42540
 A-Status: preliminary; translated from GB/EMBL/DBJ
 A-Molecule type: mRNA
 A-Residues: 1-37, 'R', 39-40, 'W', 42-91, 'S', 93-237, 'T', 239-274, 'P', 276-296, 'P', 298-393, 'G',
 A-Cross-references: UNIPARC:UPI00016904; EMBL:D89175; NID:91749557; PIDN:BAA13837.1; PIDN:BAA13837.1; P
 A-Experimental source: strain PR745
 C-Genetic:
 A-Map position: 2
 C-Function:
 A-Pathway: branched-chain amino acid biosynthesis
 C-Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase homolog
 C-Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
 F:88-274/Domain: ketol-acid reductoisomerase homology <KAR>
 Query Match 70.9%; Score 1467.5; DB 2; Length 404;
 Best Local Similarity 70.2%; Pred. No. 2.5e-102; Mis matches 64; Indels 5; Gaps 1;
 Matches 276; Conservative 48; Nucleotides 5;
 Domains 276; Conservative 48; Mis matches 64; Indels 5; Gaps 1;
 Qy 2 LRTQARLICNSRVTAKRTFALTRAAYASRPARFVKEMITDGKQINFGGTWETVY 61
 Db 14 LRTWGRS---RLATRSMVMAITAAASMRPFRMTPALMOTGRMRVMDFAGTKENW 68
 Qy 62 ERADWPREKLUYDFKNDTEALIGYGSQGYQGQLNRDNGLNVLGIVYRKOGASWKAEDEG 121
 Db 69 ERSWPREKLUYDFKNDTEALIGYGSQGYQGQLNRDQGLNVLVIVGVRKGDKASWKOALEDG 128
 Qy 122 WVKQKNUFVEDAIKRGSTYVMNLLISDAQSETPWPKPLIKTGKLYFSQGSPFPFKDLT 181
 Db 129 WPGKTLFVVEAIIKKGSTIINLLISDAQSETPWPKPLIKTGKLYFSQGSPFPFKDLT 188
 Qy 182 HVRSPKQDVLVIAVPGKSGRTVSLPKKEGRGINSYAVRDVTGKHEKAQALAVAGSG 241
 Db 189 KIRPKDQDVILVIAVPGKSGRTVRLTIFKEGRGINSFAVQDVTGKQEKAGLAVAGSG 248
 Qy 242 YVYQOTFEREVSNDIYGRGCLMGIGIHMPLAQYDVLRENGHSPSEAFNETVEATQSLY 301
 Db 249 FIVQTTPKKEVVISLVLVGERGLMGGNGFLPLAQYVQVLRRGHSPLAFNETVEATQSLY 308
 302 PLIGKQHDMYDAGSTTARGALDWYPIFKNAALKPVQFDIYESTKGNTETKRSIEFNSQ 361
 Qy 309 PLIGKQHDMYDAGSTTARGALDWYPIFKNAALKPVQFDIYESTKGNTETKRSIEFNSQ 361
 362 PYDREKLEKEDLTIRNMEIWVKVGEVKURPEN 394
 Db 369 PNTRELYDKELEETRNLWVKAGEVVRSPHE 401

ketol-acid reductoisomerase (ilvc) PAB089 - Pyrococcus abyssi (strain Orsay)
 C;Species: Pyrococcus abyssi
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
 C;Accession: HR5044
 R;anonymous, Genoscope
 Submitted to the EMBL Data Library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A;Reference number: A75001
 A;Accession: HR5044
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1332 <KAR>
 A;Cross-references: UNIPROT:Q0UZ09; UNIPARC:UPI00003453B; GB:AU248287; GB:AL096836; NID: C;Experimental source: strain Orsay
 C;Genetics:
 C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase, domain: ketol-acid reductoisomerase homology <KAR>
 Query Match 23.9%; Score 495; DB 2; Length 332;
 Best Local Similarity 38.2%; Pred. No. 1. 5e-29;
 Matches 126; Conservative 60; Mismatches 122; Indels 22; Gaps 7;
 QY 69 EKLLUDYFKNDTFALIGGSQSYQGQNLNRDGLNLNVITGVRLDGASHKAATBDGAWPGKNL 128
 Db 12 EYVSMIDLKDKTVAVIGYGNQSEAQAKMNRDGSVHVLIGLRLSSWKRAKDGF---EV 67
 QY 129 FTVEDAIKRSYVMMNLSDAQSE-T-PATKPLTKGKTYFSSHQSPSPVPLKDTVVEPK 187
 Db 68 YTIEEAKVRADLVIHILPDLQPKVYRKEVYLGFSYVPAWVQDVTGNGNADLAMAKIGCTRAVIE 124
 QY 188 DLDVILVAPKGSGRTRVSLEFKERGGRINSSYAVWNNDVTKAHKAQALAVIG--SGVYQ 245
 Db 125 YVDVILVAPKGSGRTRVSLEFKERGGRINSSYAVWNNDVTKAHKAQALAVIG--SGVYQ 245
 QY 246 TFEREVNSDLYGERQCLM3G1HGMFLAQMVNLRENGHSSEAFNETVETATQSLYPLIG 305
 Db 185 TTKRBTESLJIGEOLVLSGQELIJKGFEVPLVGLYPPFLAYFACNEA-KLIMDLIY 243
 QY 306 KYGMQMDYDAGCSTTARGALDWYPFKNAKPKVFDLYESTKTNGTETKSLF---NS 360
 Db 244 ERGFTGMLKAVSDTAKYGGITVGP-----KVIDDTVKENKKFAERVSGEFAKEWISK 297
 QY 361 QPDYRKLEKEDLTIRNMTWKGKVERKL 390
 Db 298 ADKASEVLEELMKPTEBEBIEKVGTRIKM 327

RESULT 5
 F70407 acetohydroxy acid isomerase - Aquifex aeolicus
 C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004
 C;Accession: F70407
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Reich, C.I.; Overbeek, R.; Kirnness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Sadow, P.W.; Hamma, M.C.; Cottrell, M.D.; Roberts, K.M.; Hurst, M.A.; Science 273, 1058-1073, 1996
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraer, C.M.; Smith, H.O.; Woese, C.R.; Reich, C.I.; Overbeek, R.; Kirnness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Sadow, P.W.; Hamma, M.C.; Cottrell, M.D.; Roberts, K.M.; Hurst, M.A.; A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64300; MUID:96337999; PMID:8688087
 A;Accession: F64492
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-348 <BUL>
 A;Cross-references: UNIPARC:UPI0000165FEC; GB:U67595; GB:177117; NID:91592170; PIDN:AAB9;
 C;Genetics:
 C;Map position: F01521365-152241
 C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase, domain: ketol-acid reductoisomerase homology <KAR>
 F70407
 Query Match 23.1%; Score 478; DB 1; Length 348;
 Best Local Similarity 35.3%; Pred. No. 3e-28;
 Matches 118; Conservative 67; Mismatches 125; Indels 24; Gaps 9;
 QY 66 WREKLUYFKNDTFALIGGSQSYQGQNLNRDGLNLNVITGVRLDGASHKAATBDGAWPG 125
 Db 24 YDKDVTDAVKDTIATVIGGSQSYQGQNLNRDGLNLNVITGVRLDGASHKAATBDGAWPG 125
 QY 126 KNLPLVVEDAIKRSYVMMNLSDAQSE-T-PATKPLTKGKTYFSSHQSPSPVPLKDTVVEPK 184
 Db 80 HKWVTEAEKAIDIHILPDEVQPKQKEPVYLGFSYVPAWVQDVTGNGNADLAMAKIGCTRAVIE 136
 QY 185 PPKDVLVAPKGSGRTRVSLEFKERGGRINSSYAVWNNDVTKAHKAQALAVIG--SGVYQ 242
 Db 137 PPENVNITVAPKGSGRTRVSLEFKERGGRINSSYAVWNNDVTKAHKAQALAVIG--SGVYQ 196
 QY 243 WQQTFEREVNSDLYGERQCLM3G1HGMFLAQMVNLRENGHSSEAFNETVETATQSLYPLIG 302
 Db 197 VQTQTFREETETDOLGQEVQVLCGGVTELKAFTLVAGVPMAYFETCNE-LKU1D 255
 Query Match 23.4%; Score 485.5; DB 2; Length 333;
 Best Local Similarity 35.6%; Pred. No. 7.7e-29;
 Matches 116; Conservative 64; Mismatches 129; Indels 17; Gaps 7;
 Db 256 LIYQKGLQGMWENVSNTABYGGITRARRVINEESRKAKKEILKEIQDGRFAKEWISL--- 312

RESULT 7

A96911 ketol-acid reductoisomerase [imported] - Clostridium acetobutylicum

C.Species: Clostridium acetobutylicum

C.Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004

C.Accession: A96911

C.RNOLING, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; DALY, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.; Bacteriol. 183: 4823-4838, 2001

A.Title: Genome and Comparative Analysis of the Solvent-Producing Bacterium Clc A; Reference number: A96900; MUID:21359325; PMID:21359325

A.Accession: A96911

A.Status: preliminary

A:Molecule type: DNA

A:Residues: 1-337 <KUR>

A:Cross-references: UNIPROT:Q97MW0; UNIPARC:UP10000C9D5C; GB:AE001437; PIDN:AAK78076.1;

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC0091

C,Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase

Query Match 22.7%; Score 470; DB 2; Length 337;

Best Local Similarity 36.1%; Pred. No. 1.1e-27;

Matches 122; Conservative 58; Mismatches 130; Indels 28; Gaps 10;

QY 72 LDXFKNDTIALIGYGSQYQGQNLRDGLNLVIGVRKGASHQKALEDGWPGKNUFTV 131

QY 14 LNLVLRKKLAIIGPGSQGQHANLNLKESGLNVLVLYGQSKSKWADYGF---SETEV 69

QY 132 EDAIKRGSYVMNLISDAQESTWPA-IKPLITKGKTLVFSHGSPPVFKDLTHVEPKD 190

Db 70 ADAVKRQAQVMILLPDEKQKQVIAEISKNDLDEGDLAFAHGNHNTHQIV---PPKND 126

QY 191 VILVAPKQSGRTVRSLFKEGRGINSYAWNDYTGKAHEKAQQLAVAVG--SGYVYQTF 248

Db 127 VLMIAKPGKPGHIVRRQYTEGGYFPLIYAVHQDITGKGKELIALYKGJGGTKGGWMVTF 186

QY 249 ERSVNDLIGERGCTIMGGIHMPFLAQYQVTLRENGHPSSEAFNNTVERATQSYPLIGKYG 308

Db 187 KETNDLIGEQQAVICGGICALINAGYDNTIREAGYSARNAYFFCFHE-MKMIUDLWYEGG 245

QY 309 MDYMDACSTTARGALW--PIFKQALKPVQFDLYESTKNGTETRSLEPN-SQPD 363

Db 246 MAKRYSISDTAVG--DYGWGRILINDNVRAMKVKUTEQDGTFAKWLLENQTGRPA 303

QY 364 YRKKEKELDTIRNMEIWTKVKGKEVRL-----RPNQ 395

Db 304 FNARRRIEAD---REIKVKGKLRGMMSWINENPNSNE 337

RESULT 8

AC1694 ketol-acid reductoisomerase (acetohydroxy-acid isomerase) homolog ilvc [imported]

C.Species: Listeria innocua

C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004

C.Accession: AC1694

R.Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Buchaud, E.; Durand, I.; Dussurgey, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madiheno, E.; Maitourna, A.; Ma, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Titte, Comparative genomics of Listeria species

A.Reference number: AB1077; MUID:21537279; PMID:1679669

A.Accession: AC1694

A.Status: preliminary

A:Molecule type: DNA

RESULT 10

Db 188 KETTEDIFGEQVINGGIMELMRAFAETIVEQYQPEVAFINE-LKMLVDVIEKG 246
 C;Species: Thermotoga maritima - Thermotoga maritima (strain MSBB)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004
 C;Accession: D72362
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haff, D.H.; Hickey, C.M.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Nature 39, 323-325, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A;Reference number: A72200; MUR:99287316; PMID:10360571
 A;Accession: D72362
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-336 <ARN>
 A;Cross-references: UNIPROT:Q9W220; UNIPARC:UPI000012D560; GB:AE001730; GB:AB000512; NID
 A;Experimental source: strain MSBB
 C;Genetics:
 A;Gene: TM0550
 C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase
 F;21-203/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 22.5%; Score 465; DB 2; Length 331;
 Best local Similarity 37.3%; Pred. No. 2.6e-27; Mismatches 119; Indels 32; Gaps 13; Matches 125; Conservative 59; Mismatches 119; Indels 32; Gaps 13;

Db 73 DYFKND----TRALIGQSGQYQCGNLNRDGLNGLVIGVRKOCASWKAIECDWPGK 127
 QY 8 DAVKNNALEGKTVAVIGYQSQGHANSQNLRDNGLNVIGIR-ECKSAESARNDF---D 62

Db 128 LFTVEDAIKRGSSYMMILSDAQSETWPA-AKPLIKTGKLYSHGSPSVVKLTHVEP 186
 QY 63 VYSSEAAKDAVIMILPDEPDTQETYNEKIKAGNSVFAHGFNHF-DV--INPF 119

Db 187 KDDVLVLPKGSRTVSLFKEGRGINSSYAWNDVVTGKAHEKAQALAVAGG-GYY 244
 QY 120 SDVDFVFLVPAKPGSHLVRTRFVEGAVASLPAIQDATONRDTALSYAKGIGTRAGV 179

Db 72 LDYFKNDTPALIGQSGQYQGQGQNLNRDGLNGLVIGVRKDGASHKAIDGWVPGKLNPF 131
 QY 121 LNIKDKKXIAIGYQSGOQHAKLNLKDGLSLNVVGLRAGSKSWKKAERQ---GLTVKII 67

Db 132 EDAIKRGSSYMMILSDAQSETWPA-IKPLIKTGKLYSHGSPSVVKLTHVEP KOLD 190
 QY 68 EEAKEADIMIILIPDEHOPEIYKYYIEKHLTEGKMLMFAHGENNHYHOI---PKNVD 124

Db 191 VILVAPKGSRTVSLFKEGRGINSSYAWNDVVTGKAHEKAQALAVAGG-GYYQYQTF 248
 QY 125 VTMIAPKSPGHIVRREYVEGRGPALVAVYQDVTGKAKDIALAYAKGKVTRAVIETP 184

Db 249 EREWNSDLYGERGCLMGGHGMPLAQYDLETRNGHSPSEAFNPTVEATOSYIPLIGK 308
 QY 185 KEETEDTDFGEQAVLQGTYTALKAGFETLVDAGYQPELAYFCINE-LKLTVLIVGG 243

Db 309 MDYMDAGCSTARRGALWPIFKALKVFPQDYLESTKNGIPTKRSLEP----NSQPD 363
 QY 244 LSPMRYSNTAYG--DYSQSKVLTKEVRENKQMLKDIQRGKFAKDWMLENQAGR 301

Db 364 YRKLEKELDTIRMEINVKGVKEVRKLRP 392
 QY 302 FTMRKKESEHL---IEVKVGKSLRQMP 326

RESULT 11

AB1323 ketol-acid reductoisomerase (acetohydroxy-acid isomeroeductase) homolog ilvc [imported]
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
 C;Accession: AB1323
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecher, A.; Dominguez-Bernal, G.; Duchaude, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fischi, H.;

Db 368 LB---KEADTIRMEIWKVGKVEKRL 390
 QY 302 MPTWVNGLSNVQNSLEEKIGQNLRLD 327

RESULT 12

Db 245 OTFEREVNSDLYGERGCLMGGHGMPLAQYDLETRNGHSPSEAFNPTVEATOSYIPLI 304
 QY 180 ETTKRETEETDLFQHQAVLQGATHLIOQAFETLVEAGYQPELAYFEVHE-MKLIVDLM 238

Db 305 GKGMHDYMDACSTARRGALWPIF----KHALPKVQDLYESTKNGIPTKRSLEN 359
 QY 239 YEGMMEKMHISIATYAEQYDVSQPRVUTADTKKAMKEVLTIDI---QNGNFAKSFINDN 294

Db 360 SQPYRE--KLEKELDTIRMEINVKGVKEVRKLRP 392
 QY 295 KN-GFKEFIRMKEQ---QGHQTEKVQGABLERMMP 325

RESULT 13

Db C5644 ketol-acid reductoisomerase ilvc - Bacillus subtilis
 C;Species: Bacillus subtilis
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
 C;Accession: C6644
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteletti, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chauvel, A.; Bhrlich, S.D.; Eimberger, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
 A;Authors: Feulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleguilho, J.; Harwood, C.R.; Hernaut, A.; Hilbert, H.; Hollsappel, S.; Hosono, S.; Hulio, M.F.; Koetteler, P.; Koningsstein, P.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauzees, A.; Odeiga, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portebeille, Y.; Ogawa, A.; Odeiga, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portebeille, Y.; Sato, T.; Scanlon, A.; Authors: Schlesch, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror, A.; Akauchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togomi, A.; Tosato, V.; Uchiyama, K.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshikawa, H.; Yamashita, B.; Yoshikawa, H.; Danchin, A.; Danchin, A.; Reference number: AB9580; MUID:9804033; PMID:9383377
 A;Accession: C5644
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-342 <KUN>
 A;Cross-references: UNIPROT:P37253; UNIPARC:UPI000038DEE; GB:Z99118; GB:AL009126; NID:918
 A;Experimental source: strain 168

C:Genetics:	ilvc
C:Superfamily:	ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase (21-202/Domain: ketol-acid reductoisomerase homology <KAR>)
Query Match	22.3%; Score 461; DB 2; Length 342;
Best Local Similarity	35.2%; Pred. No. 5.5e-27;
Matches	119; Conservative 68; Mismatches 115; Indels 36; Gaps 11;
QY	74 YPKND-----TPALIGYGSQYQGJNLRKGNLVIGVRKGASWKAATEEDGWV 124
Db	5 YNGDIDKENVLAGKTVAVIGVGSQHAGHLNLKSGVDVIVGIVQ-GASPTQAOED--- 59
QY	125 GKNLFTVEDAIIKRSYVMNLSIDAQSETWPA-IKPLURKGTLVFSRSPVFKDLTHV 183
Db	60 GHRKPSVKERAAQAEIIMVLPDQQQVTEAEKDELTAGKSLVPAHGFVNHFQIV-- 117
QY	184 EPPKLDVILWAPKGSGRTRVSLFEGRGRINSSAVWMDTGHKAHEKQALAYAIGSY- 242
Db	118 -PPADQVFLVAPKGPGLVLRVYBQAGVYPAFLAIYQDTGEARDKALAYAKGIGARA 176
QY	243 -WQCTPERURVNSDQIGERGQMLGIGHMLAQDVLRENGHSSEAFNETVERATOSY 301
Db	177 GYLETSTFKETETDIFGEQAVLGGSLALVKAQFTLITBAGQYQRELAYFECHLR-LKLV 235
QY	302 PLIGKVGMDYMDCSTTARGALDWY---IFKNAKRPVFDLYSTKNGRETKL 356
Db	236 DLMTVEGLAGKRYISDIAQWDFVSGPVDAKVURESPKEVLRD1---QNGJPAKEW 291
QY	357 EFN--SQPDYREKLEKELDPTIRNNEIMWIKGKVEKVKLRP 392
Db	292 VENQVNRPRFNAWSE--NEHQIEVVGKRLREMP 325
RESULT 13	
C84032	ketol-acid reductoisomerase ilvc [imported] - <i>Bacillus halodurans</i> (strain C-125)
C:Species:	<i>Bacillus halodurans</i>
C:Date:	01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
C:Accession:	C84032
R:Takami, H.; Nakabone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira	Nucleic Acids Res. 28, 4317-4331, 2000
A;Title:	Complete genome sequence of the alkaliphilic bacterium <i>Bacillus halodurans</i> and
A;Reference number:	A83650; MUID:20512582; PMID:11058132
A;Accession:	C84032
A;Status:	preliminary
A;Molecule type:	DNA
A;Residues:	1-340 <STO>
A;Cross-references:	UNIPROT:Q9K8E7; UNIPARC:UPI000012D53B; GB:AP001517; GB:BA000004; MUID:3094119
A;Experimental source:	strain C-125
C:Genetics:	ilvc
C:Superfamily:	ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase (21-229/Domain: ketol-acid reductoisomerase homology <KAR>)
Query Match	21.3%; Score 442; DB 1; Length 367;
Best Local Similarity	31.8%; Pred. No. 1.6e-5;
Matches	116; Conservative 72; Mismatches 153; Indels 24; Gaps 10;
QY	32 SRAPARFVKPMITRGLQINFRGTVIIVYERADWPRKBLIYFNDTFLALGGYGSQY 91
Db	14 SRAFAMKRSQJSTQSQ---GDSYMDMYDDANLIDLLAGKTVATIGYQ3HA 67
QY	92 QGILNTRDGLNLVIGVRKGASWKAATEDGWPGKQFLFTEDAIIKRSYVMNLSIDAQS 151
Db	68 HALNLKQSGVNUVWGLYSSKS---VAKLEG-AGLKTVAAKAAADLIMLPPBVK 123
QY	152 ETWPA-IEPLURKGTLVFSRSPVFKLTVREPKDQVILWAPKGSGRTRVSLFKEG 210
Db	124 TVEAEIAPIVNLVAGNVVLAQENINF---AIVPPRVDVMAAPKGPHVRRYEQ 180
QY	211 RGINSSYVWMDTGVKGAKBKAQALAVIGS-GYVYQTFEREVNSDLYGRRGCLMGH 268
Db	181 QGPALFVYQDQSGQARDYANAYAKIGGTRAGILETFRETTEDLFGQVVLCGJL 240
QY	249 GMFLAQDVTLRENGHSSEAFNETVEETATQSYPLIGKVGMDYMDAESTTARGALDWY 328
Db	241 ALIKAGFDTLVAQYQRELAYFECHLR-VKLIVDILVVEGLAKMRSISNTABYGLTRG 299
QY	329 P-IFKNAKRPVFDLYSTKNGRETSELEN--SQPDYREKELDTIRNNEWIKGK 385
Db	300 PRVTEETKAERQIQLDEIQSQFARFVLENQAGKPGFTAMRRSEEL---IEVGK 355

Qy : 386 EVRKLF 390
 ::| :
 Db 356 DLRAM 360

RESULT 15

F8997

alpha-keto-beta-hydroxylacil reductoisomerase [imported] - *Staphylococcus aureus* (strainC;Species: *Staphylococcus aureus*

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004

C;Accession: F8997

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Itoue, R.; Kaito, C.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Itoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.

A;Reference number: A89738; MUID:21311952; PMID:11418146

A;Accession: F8997

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-334 <KUR>

A;Experimental source: strain N315

C;Genetic:

A;Gene: ilvc

C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase

Query Match 21.3%; Score 441.5; DB 2; Length 334;

Best Local Similarity 34.1%; Pred. No. 1.5e-25; Matches 118; Conservative 68; Mismatches 125; Indels 35; Gaps 13;

Qy 59 TTYERADWPRAKLDYFKNDTFALIGYGSQGYQGLNLRDGLNNTIGVRKGASWKAAT 118

Db 3 TTY---YDQDKVTDALQGKCKIAUWGYGSQGHAAHQNLKONGYDVGIVIR-PGRSFDAK 57

Qy 119 EDGWWRPGKKNLFTVEDAIKRSQSYVMNLSDAQSEETWP-AIKPLLTKGTIVYFSIGFSPVF 177

Db 58 EDGF---DVFPAVAEVKAQDVIWILPDEIQGDVTKNEIEPNLEKHNALAFAGFNIHF 113

Qy 178 KDLTHVEPPKDLDVILWPKSGRTRSLPKGRGINSVAVMDVYTGKAHEKQALAVA 237

Db 114 --GVIQPPADAVDVEVAPKPGHLRRTTVEGSAVPSLIGTQDQASQARNTALSYAKG 170

Qy 238 IGS---GIVYQITPEREVNSDLYGERGCLMSEGIGHMPLAQDVIRNGHSPSEARNEVE 295

Db 171 IGATRAGVVIETKETEETDGFGEQAVLCCGVSKLQSGFETLVEAGYQPLAFEVLR 230

Qy 296 ATQSLVPLIGKGYMDWYDAGCSTTARRGALWY-----FIFKNAKPKVFFQDLYESTKN 348

Db 231 -MKLIVDLMVEGGMENVRYSINTAEGF--DVSQPRVITPDVKENKAVLTID----ON 283

Qy 349 GTETKRSLETFNSQPPRE--KLEKSLDTINMETMKYKVERKLRP 392

Db 284 GNFISRKFIEDKRN-GPKFVYKLRPQ--HGHQIKEYGRNREMP 325

Search completed: March 22, 2006, 15:34:33
 Job time : 21.7895 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:02 ; Search time 115.529 Seconds
 (without alignments)
 1528.885 Million cell updates/sec

Title: US-10-797-248A-1
 Perfect score: 2094

Sequence: 1 MSARGFSKALRPMARQLATP.....EIWRAGKAVRSLRPENQKQK 402

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp180s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2002s:*
- 5: geneseqp2003s:*
- 6: geneseqp2003ab:*
- 7: geneseqp2003ds:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	2094	100.0	402	6	ABR64303		Abre4303 Acetohydroxylase
2	2081	99.4	400	6	ABR64306		Abr64306 Acetohydroxylase
3	2081	99.4	400	9	ADW16807		Adw16807 M grisea
4	1856	88.6	400	6	ABR64305		Abr64305 Acetohydroxylase
5	1671	79.8	403	9	ADW16810		Adw16810 M graminicola
6	1658	79.7	396	6	ABJ26502		Abj26502 Aspergillus
7	1658	79.7	508	6	ABJ26502		Abj26502 Aspergillus
8	1634	78.0	388	6	ABJ25902		Abj25902 Aspergillus
9	1634	78.0	500	6	ABJ25877		Abj25877 Aspergillus
10	1526.5	72.9	400	4	AAU15089		Aau15089 Protein e
11	1526.5	72.9	400	5	ABP7238		Abp7238 Candida
12	1503	71.8	395	6	ABR64304		Abr64304 Acetohydroxylase
13	1503	71.8	395	7	ADK64188		Adk64188 Disease treatment
14	1421.5	67.9	409	7	ADB70124		Adb70124 C. neoformans
15	1100.5	52.6	347	6	ABU20976		Abu20976 Protein e
16	490	23.4	342	4	AAU01250		Aau01250 B. subtilis
17	475	22.7	331	5	ABB48168		Abb48168 Listeria
18	475	22.7	331	6	ABU32456		Abu32456 Protein e
19	473	22.6	332	4	AAB96356		Aab96356 Putative
20	472	22.5	337	6	ABU24174		Abu24174 Protein e
21	469	22.4	336	6	ABU15526		Abu15526 Protein e
22	468	22.3	579	2	AAY25183		Aay25183 Wheat ace
23	468	22.3	579	2	AAY25180		Aay25180 Corn ace
24	468	22.3	585	8	ADX93651		Adx93651 Plant ful

Query Match 100.0%; Score 2094; DB 6; Length 402;
 Best Local Similarity 100.0%; Pred. No. 1.4e-191;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

RESULT 1
 ID: ABR64303 standard; protein; 402 AA.
 XX

ABR64303;

XX
 AC
 DT 16-SEP-2003 (first entry)
 XX
 DE Acetohydroxyacid isomeroxidase #1.
 XX
 KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroxidase.
 XX
 OS Magnaporthe grisea.
 XX
 PR FR2829363-A1.
 XX
 PD 14-MAR-2003.
 XX
 PF 10-SEP-2001; 2001FR-00011689.
 XX
 PR 10-SEP-2001; 2001FR-00011689.
 XX
 PA (AVET) AVENTIS CROPSCIENCE SA.
 XX
 PI Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
 XX
 DR WPI; 2003-405775/39.

CC The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (1) of acetohydroxyacid isomeroxidase. (1) are used for curative or preventive treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroxidase, used to illustrate the invention

CC Sequence 402 AA;

CC Query Match 100.0%; Score 2094; DB 6; Length 402;
 CC Best Local Similarity 100.0%; Pred. No. 1.4e-191;
 CC Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSARGFSKALRPMARQLATPAVQRSSFYVASSMVRATKAAVAPTOQQIRGVATMDPAGH	60	Query Match 99.4%; Score 2081; DB 6; Length 400;
Db	1	MSARGFSKALRPMARQLATPAVQRSSFYVASSMVRATKAAVAPTOQQIRGVATMDPAGH	60	Best Local Similarity 99.8%; Pred. No. 2, 5e-190; 1; Mismatches 0; Indels 0; Gaps 0;
Qy	61	KEQWERAQWDPKELLEYFDDTIALIGGSQHGGQNLNRDNLNVITGVRDGKSWKD	120	Matches 399; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db	61	KEQWERAQWDPKELLEYFDDTIALIGGSQHGGQNLNRDNLNVITGVRDGKSWKD	120	Qy 1 MSARGFSKALRPMARQLATPAVQRSSFYVASSMVRATKAAVAPTOQQIRGVATMDPAGH 60
Qy	121	AVODGWPQKNLFFVEDEASRGTVIMNLISDAQSETWPAKQPIQTKGKTYFSSHGFSPV	180	Db 1 MSARGFSKALRPMARQLATPAVQRSSFYVASSMVRATKAAVAPTOQQIRGVATMDPAGH 60
Db	121	AVODGWPQKNLFFVEDEASRGTVIMNLISDAQSETWPAKQPIQTKGKTYFSSHGFSPV	180	Qy 61 KEQWERAQWDPKELLEYFDDTIALIGGSQHGGQNLNRDNLNVITGVRDGKSWKD 120
Qy	181	FKDLTKVEVPTDVIILCPKGSCRTVTSLFRERGINSFAYQDTGEAEKAIALGV	240	Db 61 KEQWERAQWDPKELLEYFDDTIALIGGSQHGGQNLNRDNLNVITGVRDGKSWKD 120
Db	181	FKDLTKVEVPTDVIILCPKGSCRTVTSLFRERGINSFAYQDTGEAEKAIALGV	240	Qy 61 KEQWERAQWDPKELLEYFDDTIALIGGSQHGGQNLNRDNLNVITGVRDGKSWKD 120
Qy	241	AIGSCYLYKTTFEKEVYSSLYGERGCLMCGIHGMFLAQEVLRERGHSPEAFNETVEEA	300	Qy 121 AVQDGWPQKNLFFVEDEASRGTVIMNLISDAQSETWPAKQPIQTKGKTYFSSHGFSPV 180
Db	241	AIGSCYLYKTTFEKEVYSSLYGERGCLMCGIHGMFLAQEVLRERGHSPEAFNETVEEA	300	Db 121 AVQDGWPQKNLFFVEDEASRGTVIMNLISDAQSETWPAKQPIQTKGKTYFSSHGFSPV 180
Qy	301	TQSILPLIGANGMDWMMYEACSTTARRGAIDWSPRFKDALKPQVFNQYDSDVKQSETDSL	360	Qy 121 AVQDGWPQKNLFFVEDEASRGTVIMNLISDAQSETWPAKQPIQTKGKTYFSSHGFSPV 180
Db	301	TQSILPLIGANGMDWMMYEACSTTARRGAIDWSPRFKDALKPQVFNQYDSDVKQSETDSL	360	Db 121 AVQDGWPQKNLFFVEDEASRGTVIMNLISDAQSETWPAKQPIQTKGKTYFSSHGFSPV 180
Qy	361	DYNSQPDYREKYEAEETRNLEIWRAKAVSRLENPKQK 402	400	Qy 181 FKDLTKVEVPTDVIILCPKGSCRTVTSLFRERGINSFAYQDTGEAEKAIALGV
Db	361	DYN SQPDYREKYEAEETRNLEIWRAKAVSRLENPKQK 402	400	Db 181 FKDLTKVEVPTDVIILCPKGSCRTVTSLFRERGINSFAYQDTGEAEKAIALGV
<hr/>				
RESULT 2				
ABR64306	ABR64306	standard; protein; 400 AA.		Qy 241 AIGSCYLYKTTFEKEVYSSLYGERGCLMCGIHGMFLAQEVLRERGHSPEAFNETVEEA
XX	XX			Db 241 AIGSCYLYKTTFEKEVYSSLYGERGCLMCGIHGMFLAQEVLRERGHSPEAFNETVEEA
AC	AC			Qy 301 TQSILPLIGANGMDWMMYEACSTTARRGAIDWSPRFKDALKPQVFNQYDSDVKQSETDSL
XX	XX			Db 301 TQSILPLIGANGMDWMMYEACSTTARRGAIDWSPRFKDALKPQVFNQYDSDVKQSETDSL
DT	DT			Qy 361 DYN SQPDYREKYEAEETRNLEIWRAKAVSRLENPKQK 400
XX	XX			Db 361 DYN SQPDYREKYEAEETRNLEIWRAKAVSRLENPKQK 400
DE	DE			<hr/>
XX	XX			RESULT 3
DE	DE			ADV16807 standard; protein; 400 AA.
XX	XX			XX ADV16807;
AC	AC			XX DT 24-FEB-2005 (first entry)
XX	XX			DE M grisea ketol-acid reductoisomerase IIv5 seqid 6.
DE	DE			XX substrate inhibition; antibiotic; gene disruption;
XX	XX			DE M grisea ketol-acid reductoisomerase; IIv5; enzyme.
KW	KW			XX ketol-acid reductoisomerase; IIv5; enzyme.
XX	XX			XX Magnaporthe grisea.
DE	DE			XX OS Magnaporthe grisea.
XX	XX			XX PN WO2004104176-A2.
XX	XX			XX PD 02-DEC-2004.
XX	XX			XX PD 14-MAR-2003.
XX	XX			XX PP 17-MAY-2004; 2004WO-US015404.
PF	PF			XX PR 15-MAY-2003; 2003US-0470947P.
XX	XX			XX PR 19-MAY-2003; 2003US-0471615P.
PR	PR			XX PR 21-MAY-2003; 2003US-0472242P.
XX	XX			XX (PARA-) PARADIGM GENETICS INC.
PA	PA			XX PA Tanzer MM, Hamer L, Adachi K, Deenzaan TM, Lo SC; Heiniger RW;
PA	PA			XX PI Montenegro-Chamorro MV, Darveaux BA, Frank SA, Heiniger RW;
XX	XX			XX PI Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;
XX	XX			XX DR WPI; 2005-021202/02.
XX	XX			XX DR N-PSDB; ADV16805, ADV16806.
CC	CC			XX PT Identifying a test compound as a candidate for an antibiotic comprises
CC	CC			PT contacting ornithine carbamoyltransferase (OCTase) or ketol-acid
CC	CC			PT reductoisomerase polypeptide, or fungal pathogenicity-conferring gene
CC	CC			XX with a test compound.
SQ	SQ			XX Claim 48; SEQ ID NO 6; 179pp; English.
PS	PS			PS

XX The invention describes a method of identifying a test compound as a candidate for an antibiotic comprising contacting ornithine carbamoyltransferase (Ocrase) or ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound. The method comprises contacting OCT-1 gene polypeptide, ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound ; and detecting the presence or absence of binding between the test compound and the polypeptide or gene, where binding indicates that the test compound is a candidate for an antibiotic. Also described are: an isolated nucleic acid comprising a nucleotide sequence encoding a polypeptide having at least 50% sequence identity to, or having at least 10% of the activity of, 400, 403 or 469 amino acids; and an isolated polypeptide comprising essentially the amino acid sequence of 400, 403 or 469 amino acids. The methods are useful for identifying inhibitors of ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal pathogenicity-conferring gene as antibiotics. This is the amino acid sequence of Magnaporthe grisea ketol-acid reductoisomerase ILV5.

XX Sequence 400 AA;

Sequence Match 99.4%; Score 2081; DB 9; Length 400;

Best Local Similarity 99.8%; Pred. No. 2.5e-190; Mismatches 1; Indels 0; Gaps 0;

XX Matches 399; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query 1 MSARGFSKALRPMARQLAPAVQRSSFVAASSMYTRAKAVAPTQQQIRGVKIMDFAGH 60
 Db 1 MSARGFSKALRPMARQLAPAVQRSSFVAASSMYTRAKAVAPTQQQIRGVKIMDFAGH 60
 Db 61 KEQWPERADWPKKEKLEFFKDDTLALIGGSQGHGQCLNLIRDNGLNVLIGVRKDGSKWD 120
 Db 61 KEQWPERADWPKKEKLEFFKDDTLALIGGSQGHGQCLNLIRDNGLNVLIGVRKDGSKWD 120
 Qy 121 AVQDQWVPGNLFEVDEAISRGTVIMNLSSDAQSETWALKPQITKGKLYSHGFSPV 180
 Db 121 AVQDQWVPGNLFEVDEAISRGTVIMNLSSDAQSETWALKPQITKGKLYSHGFSPV 180
 Qy 181 FKDLTKEVETDIDVILCAPKGSCTRVSLFREGRGINSFSAYQDVTGEAEKAIALGV 240
 Db 181 FKDLTKEVETDIDVILCAPKGSCTRVSLFREGRGINSFSAYQDVTGEAEKAIALGV 240
 Qy 241 AIGSGYLYKTTFEKEVYSDIYGERGCLMCGSIHGMFLAQEVYLBERGHSSSEAFNETVEA 300
 Db 241 AIGSGYLYKTTFEKEVYSDIYGERGCLMCGSIHGMFLAQEVYLBERGHSSSEAFNETVEA 300
 Qy 301 TQSILPLIGANGMDWYEAFCSTTARGAIDWSPRFKDAKLPVNQLYSVKQDSETQSL 360
 Db 301 TQSILPLIGANGMDWYEAFCSTTARGAIDWSPRFKDAKLPVNQLYSVKQDSETQSL 360
 Qy 361 DYNQDPTREKYEAEEMEEIRNLIEWRAGKAVRSLRPENOK 400
 Db 361 DYNQDPTREKYEAEEMEEIRNLIEWRAGKAVRSLRPENOK 400
 Qy 400 DYNQDPTREKYEAEEMEEIRNLIEWRAGKAVRSLRPENOK 400
 Db 400 DYNQDPTREKYEAEEMEEIRNLIEWRAGKAVRSLRPENOK 400

RESULT 4
 ABR64305 standard; protein; 400 AA.
 XX
 AC ABR64305;
 XX DT 16-SEP-2003 (first entry)
 XX DE Acetohydroxyacid isomerase.
 XX KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomerase.
 XX OS Neurospora crassa.
 XX PN FR2829363-A1.
 XX PD 14-MAR-2003.
 XX PR 10-SEP-2001; 2001FR-00011689.

XX PR 10-SEP-2001; 2001FR-00011689.
 XX PA (AVET) AVENTIS CROPSCIENCE SA.
 XX Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
 XX WPI, 2003-40575/39.
 XX DR Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid isomerase.
 XX PT
 XX PT
 XX PT
 XX PS Claim 2; Fig 1; 66pp; French.
 XX CC The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomerase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomerase, used to illustrate the invention
 CC Sequence 400 AA;
 XX SQ Sequence 400 AA;
 Query Match 88.6%; Score 1856; DB 6; Length 400;
 Best Local Similarity 86.8%; Pred. No. 9.6e-169;
 Matches 349; Conservative 35; Mismatches 14; Indels 4; Gaps 2;
 Qy 1 MSARGFSKALRPMARQLAPAVQRSSFVAASSMYTRAKAVAPTQQQIRGVKIMDFAGH 58
 Db 1 MSARGFSKALRPMARQLAPAVQRSSFVAASSMYTRAKAVAPTQQQIRGVKIMDFAGH 58
 Db 1 MAARNCTALRPLARQLAPAVQRSSFVAASSMYTRAKAVAPTQQQIRGVKIMDFAGH 60
 Qy 59 GHKEQWPERADWPKKEKLEFFKDDTLALIGGSQGHGQCLNLIRDNGLNVLIGVRDGKSW 118
 Db 61 GHKEBVERADWPKKEKLEFFKDDTLALIGGSQGHGQCLNLIRDNGLNVLIGVRDGKSW 120
 Qy 119 KDAVQDGHGPVPGNLFEVDEAISRGTVIMNLSSDAQSETWALKPQITKGKLYSHGFS 178
 Db 121 EDAIQDGWVPGNLFEVDEAISRGTVIMNLSSDAQSETWALKPQITKGKLYSHGFS 180
 Qy 179 PFKDLTKEVETDIDVILCAPKGSCTRVSLFREGRGINSFSAYQDVTGEAEKAIALGV 238
 Db 181 PFKDLTKEVETDIDVILCAPKGSCTRVSLFREGRGINSFSAYQDVTGEAEKAIALGV 240
 Qy 239 GVAIGSGYLYKTTFEKEVYSDIYGERGCLMCGSIHGMFLAQEVYLBERGHSSSEAFNETVEA 298
 Db 241 GVAIGSGYLYKTTFEKEVYSDIYGERGCLMCGSIHGMFLAQEVYLBERGHSSSEAFNETVEA 300
 Qy 301 EATQSLPLIGANGMDWYEAFCSTTARGAIDWSPRFKDAKLPVNQLYSVKQDSETQSL 360
 Db 301 EATQSLPLIGANGMDWYEAFCSTTARGAIDWSPRFKDAKLPVNQLYSVKQDSETQSL 360
 Qy 359 SLIDYNSQDPTREKYEAEEMEEIRNLIEWRAGKAVRSLRPENOK 400
 Db 361 SLIDYNSQDPTREKYEAEEMEEIRNLIEWRAGKAVRSLRPENOK 400
 RESULT 5
 ID ADV16810 standard; protein; 403 AA.
 XX AC ADV16810;
 XX AC ADV16810;
 XX DT 24-FEB-2005 (first entry)
 XX DE M graminicola ketol-acid reductoisomerase KARI seqid 9.
 XX KW substrate inhibition; antibiotic; gene disruption;
 XX KW ketol-acid reductoisomerase; KARI; enzyme.
 XX OS Nycosphaeraella graminicola.
 XX PN WO2004104176-A2.

XX 02-DEC-2004. Qy 357 QESLDNNSQPDYREKTAEMEBIRNLBIWRAGKAVRSLRPEN 398
 XX 17-MAY-2004; 2004IWO-US015404. Db 361 QPTMEYAGRKYTEAEMEBIRNLBIWRAGKAVRSLRPEN 402
 XX
 PR 15-MAY-2003; 2003IHS-0470947P. RESULT 6
 PR 19-MAY-2003; 2003IHS-047115P. ID ABJ26477 standard; protein; 396 AA.
 XX 21-MAY-2003; 2003IUS-0472242P.
 PA (PARA-) PARADIGM GENETICS INC. XX
 PI Tanzer MM, Hamer L, Adachi K, Dezaan TM, Lo SC; Heiniger RW; Montenegro-Chamorro MV, Darveaux BA, Frank SA, Heiniger RW; Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR; DR WPI; 2005-021202/02. XX
 PI Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoyltransferase (OCTase) or keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound. PT DR
 PT Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoyltransferase (OCTase) or keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound. PT DR
 PT Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoyltransferase (OCTase) or keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound. PT DR
 PT Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoyltransferase (OCTase) or keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound. PT DR
 PT Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoyltransferase (OCTase) or keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound. PT DR
 PT Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoyltransferase (OCTase) or keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound. PT DR
 PT Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoyltransferase (OCTase) or keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound. PT DR
 PS Claim 50; SEQ ID NO 9; 179pp; English.
 XX The invention describes a method of identifying a test compound as a candidate for an antibiotic comprising contacting ornithine carbamoyltransferase (OCTase) or keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound. The method comprises: contacting OCTase polypeptide, keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound ; and detecting the presence or absence of binding between the test compound and the polypeptide or gene, where binding indicates that the test compound is a candidate for an antibiotic. Also described are: an isolated nucleic acid comprising a nucleotide sequence encoding a polypeptide having at least 50% sequence identity to, or having at least 10% of the activity of, 400, 403 or 469 amino acids, and an isolated polypeptide consisting of the amino acid sequence of 400, 403 or 469 amino acids. The methods are useful for identifying inhibitors of ornithine carbamoyltransferase, keto-acid reductoisomerase, and fungal pathogenicity-confering gene as antibiotics. This is the amino acid sequence of *Mycosphaerella graminicola* keto-acid reductoisomerase KARI. XX
 SQ Sequence 403 AA;
 Query Match 79.8%; Score 1671; DB 9; Length 403;
 Best Local Similarity 78.4%; Prcd. No. 5.4e-15; Mismatches 40; Conservative Matches 315; Indels 4; Gaps 1;
 Qy 1 MSARGFSK2LRPMQLATPAVQRSSVTAASSMVRAT---RKAAVAPQQQIGVKTMD 56
 Db 1 MASKNATRALARSLRQLKAPQVQRSVFAAVNARSPVSLPAQAVTAFFQVQYRGAKTV 60
 Qy 57 FAGHKEQWERADWPKEKLEYFDDTLALIGYSGQHGGQHGGQHGGQHGGQHGG 116
 Db 61 FAGDKERYFDDMPREKLEYFDDTLALIGYSGQHGGQHGGQHGGQHGGQHGG 120
 Qy 117 SWKDAVQDNWPGKNLFEDVDEAISRGTVIIMNLISDAQSETWPKQPTKTKLYPSHG 176
 Db 121 SWKEAEGDQWVEGKNLFDQDTAIGKGTIMNLISDAQSETWPKHOMLTKTKLYPSHG 180
 Qy 177 FSPYFKDQLTKEVPTDWDVLCAPKGSGRTVRSLFREGRGINSSPAVYQDTGEAEKAI 236
 Db 181 FSPYFKDQLTKEVPTDWDVLCAPKGSGRTVRSLFREGRGINSSIAFQDVTGKAEEKAI 240
 Qy 237 ALGAIGSCSYLYKTFEGEVSYLIGYSGQHGGQHGGQHGGQHGGQHGGQHGG 296
 Db 241 ALGAIGAVGSSYMMKTFERKVSYLIGYSGQHGGQHGGQHGGQHGGQHGGQHGG 300
 Qy 297 VEEATQSLYPLIGNGMDMVEACSTTARGAIDWSPFKDALKPVNQLYDSVKDSET 356
 Db 301 VEEATQSLYPLIGNGMDMVEACSTTARGAIDWSPKRFKETLKPVFEELDSVKTGKET 360

XX 357 QESLDNNSQPDYREKTAEMEBIRNLBIWRAGKAVRSLRPEN 398
 XX 361 QPTMEYAGRKYTEAEMEBIRNLBIWRAGKAVRSLRPEN 402
 XX
 RESULT 6
 ID ABJ26477 standard; protein; 396 AA.
 XX
 AC ABJ26477;
 DT 16-APR-2003 (first entry)
 XX
 Aspergillus fumigatus essential gene protein #1135.
 DE Fungicide; cytostatic; essential gene; *Aspergillus fumigatus*; infection; cancer; contamination; biofilm; antibody; immune response.
 XX
 KW Aspergillus fumigatus
 XX
 DE Aspergillus fumigatus
 XX
 OS Aspergillus fumigatus
 XX
 PN WO200286090-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013142.
 XX
 PR 23-APR-2001; 2001US-0285657P.
 PR 27-APR-2001; 2001US-0287068P.
 PR 05-JUN-2001; 2001US-0295890P.
 PR 09-JUN-2001; 2001US-0303899P.
 PR 31-AUG-2001; 2001US-0316362P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Jiang B, Tishoff D, Zamudio C, Broshkin AM, Hu W, Lemieux SM;
 XX DR WPI; 2003-093124/08.
 XX
 PT New purified or isolated nucleic acids of essential genes of *Aspergillus fumigatus*, useful for treating or preventing infections by *A. fumigatus*, or for treating a non-infectious disease in a subject e.g. cancer.
 XX
 PS Disclosure; Page; 175pp; English.
 XX
 CC The invention relates to novel purified or isolated nucleic acids of essential genes of *Aspergillus fumigatus*. The isolated nucleic acids of the invention are used to treat or prevent non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by *A. fumigatus*, or to prevent or inhibit formation of a biofilm comprising *A. fumigatus*. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of *A. fumigatus* to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case of virulence factors. This sequence represents a protein of one of the essential genes of *Aspergillus fumigatus* of the invention
 XX
 SQ Sequence 396 AA;

Query Match	79.7%	Score 1668;	DB 6;	Length 396;
Best Local Matches	79.1%	Pred. No. 1e-150;		
Matches	318;	Conservative	42;	Mismatches 34;
		Indels	8;	Gaps 4;
1	MSARGFSKALRPMAROLATPAVQRRESFVAASSMVRATKAA--VAPTOQQIRGVKTMDEA	58		
1	MASTRGLPRAK-L-VAAP---RIVSIALAIPRPLAKAATRVAASSTAPVRGVKTAFA	54		
59	GHKEQWERAADWPKEPKLLEYPKDDTLALIGYGSQGHCQGLNLIRDNGLNIVI1GIVRKDGKSW	118		
55	DSKETTYERADWPREKQYEPKNDTLALIGYGSQGHCQGLNLIRDNGLNIVI1GIVRKDGKSW	114		
119	KDAVQDGWVPSKNLFEVDEA1SRGTVIMNLISDAQSETWPLKPKITGKTLYFSGFS	178		
115	KEA1QDGWVPSKNLFDLTFEYQKGTVIWMNLISDAQSETWPLKPLITKGKTLYFSGFS	174		
179	PVFKDILTKVEVPTDIDVILCAPKGSQRTVRSLFREGRGINSFAYQDVTGAEAKIAL	238		
175	PVFKEJTKVDPKDVILVAPKGSQRTVRLFREGRGINSIAVYQDVTGAEAKIAL	234		
239	GVAIGSGLYLKTIFKEVYSDLYGERGCLMGGIHMGLQAYEVLRGRHSPSEAFNETVE	298		
235	GVAVSGLYLKTTFKEVYSDLYGERGCLMGGIHMGLQAYEVLRGRHSPSEAFNETVE	294		
299	BATQSIYPLIGANGHDWYIACSTTARRGAIDWSPEPKDALKPENQLYDSVKGSETQR	358		
295	BATQSIYPLIGANGHDWYIACSTTARRGAIDWSSEPKDALKPENLYDSVKGSETQR	354		
359	SLDYNQSDPYREKYEAEEMEIRNLIEWRAKGAVRSLRPENQ 400			
CC	essential genes of <i>Aspergillus fumigatus</i> . The isolated nucleic acids of			
CC	the invention are used to treat or prevent infections by a pathogenic			
CC	organism such as <i>A. fumigatus</i> , to treat a non-infectious disease in a			
CC	subject (e.g. cancer), to prevent or contain contamination of an object			
CC	by <i>A. fumigatus</i> , or to prevent or inhibit formation on a surface of a			
CC	biofilm comprising <i>A. fumigatus</i> . The polynucleotides are useful for			
CC	expressing recombinant protein for characterisation, screening or			
CC	therapeutic use as markers for host tissues in which the pathogenic			
CC	organism invades or resides, for comparing with the DNA sequence of <i>A.</i>			
CC	<i>fumigatus</i> to identify duplicated genes or paralogues having the same or			
CC	similar biochemical activity and/or function, for comparing with DNA			
CC	sequences of other related or distant pathogenic organisms to identify			
CC	potential orthologous essential or virulence genes, for selecting and			
CC	making oligomers for attachment to a nucleic acid array for examination			
CC	of expression patterns, for raising anti-protein antibodies, as an			
CC	antigen to raise anti-DNA antibodies or to elicit another immune			
CC	response, and for identifying polynucleotides encoding the other protein			
CC	with which binding occurs or to identify inhibitors of the binding			
CC	interaction. The polypeptides may be used to raise antibodies or to			
CC	elicit immune response, as a reagent in assays designed to quantitatively			
CC	determine levels of the protein in biological fluids, as a marker for			
CC	host tissues in which pathogenic organism invades or resides, and to			
CC	isolate correlative receptors or ligands in the case of virulence			
CC	factors. This sequence represents a protein of one of the essential genes			
CC	of <i>Aspergillus fumigatus</i> of the invention			
XX	Sequence 508 AA;			
SQ	Query Match 79.7%; Score 1668; DB 6; Length 508;			

QY	1	MSARGFSTALRPMARQLATPAVORRSFYAASSMVRATKAA- -VAPTOQQIQRGYTMDFE 58
Db	113	MASRGLPMLR-LAR-VAAP- -RTVISAALPRLAKAATRVASTA PVRGTVIAFA 166
QY	59	GHKEQWNERADWPKKEKLLYFKDTTLALIGYGSQHGGQCLNLRONGLNLVIGVRKDGSW 118
Db	167	DSKETVVERADWPREKQEFKNDTLALIGYGSQHGGQCLNLRONGLNLVIGVRKDGSW 226
QY	119	KDAVQDGIVPGPKOLFEDVAISGTVIINLLSDA QSETWPAKXQPIITKGKTLFVSHGFS 178
Db	227	KEAIQDGWIPGKNLFDLTAVQKGTVINLLSDA QSETWPAKXQPIITKGKTLFVSHGFS 286
QY	179	PVKFDLTKEVPIPDVDTLCAPKGSGRTVSLFREGRINSSPAVYDVTGEAEKIAI 238
Db	287	PVKFELTKDVPKDVDTLCAPKGSGRTVSLFREGRINSSPAVYDVTGEAEKIAI 346
QY	239	GVAIGSGYLYKTFEKEYVSDLYGERGCLMGGTHGMFLAQYEYVLRERGHSPSEANETV 298
Db	347	GVAIGSGYLYEFTFEKEYVSDLYGERGCLMGGTHGMFLAQYEYVLRERGHSPSEANETV 406
QY	299	EAQSILYPLIGANGMDMMYEACSTTARGAIDMSPRFEDALKPVNPOLYDSVKDQSETQR 358
Db	407	EAQSILYPLIGANGMDMMYEACSTTARGAIDMSPRFEDALKPVNPOLYDSVKDQSETQR 466
QY	359	SLDYNNSQDREYKEAEMEBIRNLIEWRAGKAVSRLRPPNQK 400
Db	467	SLEYNSQDREYKEAEMDIRDLEWRAGKAVSRLRPPNQK 508
16-APR-2003 (First entry)		
Aspergillus fumigatus essential gene protein #1160.		
Aspergillus fumigatus, cyrostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response.		
Aspergillus fumigatus.		
W0200286090-A2.		
31-OCT-2002.		
23-APR-2002; 2002W0-US013142.		
23-APR-2001; 2001US-0285697P.		
27-APR-2001; 2001US-0287066P.		
05-JUN-2001; 2001US-0295690P.		
09-JUL-2001; 2001US-0303899P.		
31-AUG-2001; 2001US-0316362P.		

Aspergillus fumigatus.	Db	175	PVFKETKVDPKDGVILVAPKGGRTVTLFRGRGINSIAYQDYGKAKIAJ
WO200206090-A2.	Qy	239	GVAIGSGYLYKTTKEKEVYSDLYGRGCLMGGIHMELAQEYVLERGHSPSEARNETVE
31-OCT-2002.	Db	235	GVAVGGYLYTETTFFKEEVYSDLYGRGCLMGGIHMELAQEYVLERGHSPSEARNETVE
PP 23-APR-2002; 2002WO-US013142.	Qy	299	BATQSIYPLIGANGDWMYFACSTARGAIDWSPRFKDALIKPVENQLYDSVQDSETQR
XX	Db	295	EATQSIYPLIGANGDWMYAACTTARRGAIDWSPRFKDALIKPVENQLYDSVQDSETQR
PR 23-APR-2001; 2001US-0285697P.	Qy	359	SLDYNISQPDYREKTYEMETIRNIEIWRAGKAVR
PR 05-JUN-2001; 2001US-0287056P.	Db	355	SLEYNSQDYREKTYEMODIRLIEIWRAGKAVR
PR 09-JUL-2001; 2001US-0303899P.	Qy	392	
PR 31-AUG-2001; 2001US-0316362P.	Db	388	
XX			
ELITRA PHARM INC.			
XX			
Jiang B, Tishkoff D, Zamudio C, Broshkin AM, Hu W, Lemieux SM;			
XX			
DR WPI; 2003-093124/08.			
XX			
PT New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.			
PT			
XX			
PS Disclosure: Page: 175pp; English.			
XX			
CC The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention.			
CC			
CC Sequence 388 AA;			
CC			
CC Query Match 78.0%; Score 1634; DB 6; Length 388;			
CC Best Local Similarity 78.9%; Pred. No. 1..8e-147;			
CC Matches 311; Conservative 42; Mismatches 33; Indels 8; Gaps 4;			
Qy 1 MSARGFSKALRPMAROLATPAVORRSFAVASSMYVRATKAA-YAPTOQOIRGYKTMDDA 58			
Qy 1 MASRGFLPRA-LAR-VAAP---RTVISAALPRLAATRAVAATSPVRGVKTIATA 54			
Qy 59 GHKEQWWERADWPKEKLLPEYKFDOTLALYQGSGQHGGQINLRDGLNLTIGRKDGKSW 118			
Qy 55 DSKETTYERADWPKEKLLPEYKFDOTLALYQGSGQHGGQINLRDGLNLTIGRKDGKSW 114			
Db 119 KDAQDGVWPKRNLPFEDVIAISLQYKTMDDAQAQSETWPALKPQTIGKTLYFSGHGS 178			
Qy 115 KEAQDGVWPKRNLPFUDTEAVQKGTVIWNILSQAQSETWPALKPQTIGKTLYFSGHGS 174			
Db 119 PVEFKDLTKEVPTDYLIVAPKGGRTVTLFRGRGINSIAYQDYGKAKIAJ			

CC with which binding occurs or to identify inhibitors of the binding
 CC interaction. The polypeptides may be used to raise antibodies or to
 CC elicit immune response, as a reagent in assays designed to quantitatively
 CC determine levels of the protein in biological fluids, as a marker for
 CC host tissues in which pathogenic organism invade or reside, and to
 CC isolate correlative receptors or ligands in the case or virulence
 CC factors. This sequence represents a protein of one of the essential genes
 XX of *Aspergillus fumigatus* of the invention

Sequence 500 AA;

Query Match 78.0%; Score 1634; DB 6; Length 500;
 Best Local Similarity 78.9%; Pred. No. 2.7e-147; Matches 311; Conservative 42; Mismatches 33; Indels 8; Gaps 4;
 CC

Qy 1 MSARGFSKALRPMARQLATPAVQRSSVFAASSMVRATRKA- -VAPTOQQIRGVKTMDDA 58
 Db 113 MASGRGLPRLR-LAR-VAAP- -RTVISAALPRPLAKATRVAASPAVPGVKTIAA 166
 Qy 59 GHKEQWVWERADWPKEKLEPKDQTLALIGYSGOHHGCGQGLNLDRQGLNLTVGVRDGKSW 118
 Db 167 DSKETYERADWPKEKLEPKDQTLALIGYSGOHHGCGQGLNLDRQGLNLTVGVRDGKSW 226
 Qy 119 KDAVQDGWPGSKNLPEVDEAISRGTVIIMNLISDAQSETTPNPAKQITKCKTLYFSHGS 178
 Db 227 KEAIQDGWPGSKNLPEVDEAISRGTVIIMNLISDAQSETTPNPAKQITKCKTLYFSHGS 286
 Qy 179 PVEFDLTKVEPTDIDVILCPAKGSGRTVSLFRGRGNSFAYVQDTGEAEKAFA 238
 Db 287 PVEKELITKDVPKDIDVILCPAKGSGRTVSLFRGRGNSFAYVQDTGEAEKAFA 346
 Qy 239 GVAIGSGYLYKTTFEKEVSDYLYERGCLMGGTHMELAQEVYLERGHSPSEAFNETTE 298
 Db 347 GVAIGSGYLYKTTFEKEVSDYLYERGCLMGGTHMELAQEVYLERGHSPSEAFNETTE 406
 Qy 299 EATOSLYPLIGANGMDMMYEAACSTTARRGAIDWSPRKFQALKPYNQNLDSVRDGSETOR 358
 Db 407 EATOSLYPLIGANGMDMMYEAACSTTARRGAIDWSPRKFQALKPYNQNLDSVRDGSETK 466
 Qy 359 SLDIINQDREKYEAEEMTEIRNLIWRAGKAVR 392
 Db 467 SLEYNSQDOKTREKYEKEMQDIDRLEIWRAGKAVR 500

RESULT 10
 AAU15089

ID AAU15089 standard; protein; 400 AA.
 XX

AAU15089;

DT 04-DEC-2001 (first entry)

DB Protein encoded by *C. albicans* essential gene CAYLR355C (ILV5).

XX Gene identification; essential gene; GRACE; pathogenic fungus;
 KW Gene replacement and conditional expression; fungal infection.
 XX

OS *Candida albicans*.

XX

PN WO200160975-A2.

XX

PD 23-AUG-2001.

XX

PP 20-FEB-2001; 2001W0-US005551.

XX

PR 18-FEB-2000; 2000US-0163534P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Roemer T, Jiang B, Boone C, Bussey H;

XX

WPI: 2001-489080/53.

DR N-PSDB; AAS23417.

DR

11-JUL-2002.

XX PT Identifying genes essential to fungal metabolism and identifying potential therapeutic agents that target these genes.
 PT XX

PS Claim 43; Page 222-223; 324bp; English.

XX

CC The present invention relates to novel methods for constructing fungal

CC strains useful for identification and validation of gene products as

CC targets for therapeutic agents, for creating a collection of identified

CC essential genes, and screening assays for the discovery of new drugs. The

CC invention provides the GRACE (gene replacement and conditional

CC expression) method for the construction of mutant organisms referred to any

CC ASGRACE strains of the organism. The invention can be applied to any

CC organism, particularly a pathogenic fungus e.g. *Candida albicans*,

CC *Aspergillus fumigatus* and *Cryptococcus neoformans*. The methods are useful

CC to identify agents that may be used in the treatment of fungal

CC infections. AAU15053-AAU15113 represent proteins encoded by *C. albicans*

CC essential genes.

XX

Sequence 400 AA;

XX

CC

XX	26-DEC-2001; 2001WO-US049486.	Db	300 EATQSLPLIGYGMDDYDACSTTARRGALDWPRFKDALKPVFPELYESVNGSETKR 359
XX	29-DEC-2000; 2000US-0259128P.	Qy	359 SLDYNNSPDYREKYEAEEMEIRNLLEITRAGKAVRSRPNQ 39
PR	20-FEB-2001; 2001US-00792024.	Db	360 SLEFNRSRSDYKLERLEELQTENMEIWRGCEVKRPNQ 400
PR	22-AUG-2001; 2001US-0314050P.		
XX	(BLIT-) BLITRA PHARM INC.		
PA	PA		
XX	Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;		
PI	WPI; 2002-566694/60.		
XX	DR N-PDB; ABZ31788.		
XX	Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.		
PS	Claim 44; SEQ ID NO 7075; 167pp + Sequence Listing; English.		
XX	The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of <i>C. albicans</i> cells and for treating infection by <i>C. albicans</i> . The present sequence is that of an essential <i>Candida albicans</i> protein used in the method of the invention.		
CC	Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office		
XX	Sequence 400 AA;		
Qy	1 MSARGFSKALRPMQLATPAVQRSSFW-ASSMVRATRKAAVAPTO-QQIRGVKIMDFA 58	Query Match	71.8%; Score 1526.5; DB 5; Length 400;
Best Local Similarity	72.9%	Best Local Similarity	71.8%; Score 1503; DB 6; Length 395;
Matches	296; Conservative 49; Mismatches 53; Indels 3; Gaps 3;	Matches	72.9%; Pred. No. 6.8e-135; Pred. No. 6.8e-135;
SQ		3;	
Db	1 MSPRTTSMRMLATAKATLSKRTFSLLANATRTYTAASSAKMTPTISRGVKTINF 60	Qy	10 LRPMAROL--ATPAVQRSSFWAASSMVRATRKA--VAPTQQQIRGVKIMDFAGHKEQV 64
Qy	59 GHEQQVWEADWPWKEKLLEFYDVAISRTVIMNLLSDAQSTWPALKPQITKGKTLFSGFQS 118	Db	2 LRTQARLICNSRVITAKTFLATRAAAYSRPAAFRVKP-MITTRGLKQINFGGTVETV 60
Db	61 GTEEVVHEADWPWKEKLLEFYDVAISRTVIMNLLSDAQSTWPALKPQITKGKTLFSGFQS 119		
Qy	119 KDAVQDGWYNGPKNLFYDVAISRTVIMNLLSDAQSTWPALKPQITKGKTLFSGFQS 178	Qy	65 WERADWPKEXKLLEFYDFTTLALIGYSQGHGGLNARDNGNVIIGRKDQKSWKAVQD 124
Db	120 EAAVBDGWPGENLFYDVAISRTVIMNLLSDAQSTWPALKPQITKGKTLFSGFQS 179	Db	61 YERADWPKEXKLLEFYDFTTLALIGYSQGHGGLNARDNGNVIIGRKDQGASWKAIAED 120
Qy	179 PVEKDILTKEVPTDWDVILCAPKGSGRTVSLFREGCINNSPAVQDTGAAEKAIAL 238	Qy	125 GIVPGKQNLPEVDEAISRGTVIMNLLSDAQSTWPALKPQITKGKTLFSGFSPVKD 184
Db	180 PVEKDILTKEVPTDWDVILCAPKGSGRTVSLFREGCINNSPAVQDTGAAEKAIAL 239	Db	121 GIVPGKQNLPEVDEAISRGTVIMNLLSDAQSTWPALKPQITKGKTLFSGFSPVKD 180
Qy	239 GVAIGSGYKXKTFKEVYSDYLGRCGIMGGHGMFLAQEVYLRGHSPEAFNETVE 298	Qy	185 TKEVPTDWDVILCAPKGSGRTVSLFREGCINNSPAVQDTGAAEKAIALGAIGS 244
Db	240 AIAIGSGYKXKTFKEVYSDYLGRCGIMGGHGMFLAQEVYLRGHSPEAFNETVE 299	Db	181 TKEVPTDWDVILCAPKGSGRTVSLFREGCINNSPAVQDTGAAEKAIALGAIGS 240
Qy	299 EATQSLPLIGYGMDDYEAESTARRGAIMDSPRFKDALKPVFPELYESVNGSETKR 358	Qy	245 GIVLYKTTFEKEVYSDYLGRCGIMGGHGMFLAQEVYLRGHSPEAFNETVEATQSL 304

Db	241	GIVYQCTTPEVERNSDLYGERGLMMGGTHGMFLAQDVLENGHSSEAFNFTVEATQSL	300		Matches 288; Conservative 45; Mismatches 56; Indels 6; Gaps 3;
Qy	305	YPLIGANGMDMYEASTTARGTDWSPRFDAKPVFNLQYDVKDGETQRSLDYS	364	Qy 10 LRPMPQL--ATPAVQRQRSFVAASSMVRATKAA--VAPTPQQQRGVYKTMDFAGHCKEQV 64	
Db	301	YPLIGANGMDMYEASTTARGTDWSPRFDAKPVFNLQYDVKDGETQRSLDYS	360	Db 2 LRTQBARLICNSRVTAATPFLAATRAAAYSRPAPRFVKP-MITRGLKQINFSGTCTVRY 60	
Qy	365	QPDYREKYEAEEMEEIRNLINTRAGKAVRSLRPNQ	399	Qy 65 WERADWPKEKLLFVFDLTLALIGGSQHGOGLNLRDNGLNTIGVRKDGSMDAYD 124	
Db	361	QPDYREKYEAEEMEEIRNLINTRAGKAVRSLRPNQ	395	Db 61 YERADWPKEKLLFVNDPFLALIGGSQHGOGLNLRDNGLAVIGVRKDGSMDAYD 120	
RESULT 13					
ADK64188					
ID	ADK64188	standard; protein; 395 AA.			
XX	AC	ADK64188;			
DT	06-MAY-2004	(first entry)			
XX	Disease	treating protein complex-derived protein #1281;			
XX	KW	protein complex; drug target; diagnosis.			
XX	OS	Unidentified.			
XX	EP1338608-A2.				
PN	27-AUG-2003.				
PD	20-DEC-2002;	2002EP-00102902.			
XX	PR	20-DEC-2001;	2001EP-00130253.		
XX	PA	(CELL-) CELLZONE AG.		RESULT 14	
XX	PA	Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;		ADB70124	
PI	PI	Marzloch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;		ID	ADB70124 standard; protein; 409 AA.
PI	PI	Michon A, Leutwein C, Rick J;		XX	
XX	XX	WPI; 2003-638460/61.		AC	ADB70124;
DR	DR	N-PSDB; ADK64189.		DT	04-DEC-2003 (first entry)
XX	XX	New proteins and protein complexes from eukaryotes, useful as targets in drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or disorder in a subject.		XX	C. neoformans amino acid sequence SEQ ID NO:3168.
PS	PS	Disclosure; SEQ ID NO 2561; 13pp; English.		DB	C. neoformans fungicide; gene therapy; infection.
XX	PA	The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologe or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs or pharmaceuticals for the treatment or preventing a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).		OS	Cryptococcus neoformans.
XX	CC	The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologe or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs or pharmaceuticals for the treatment or preventing a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).		XX	OS
XX	CC	Sequence 395 AA;		XX	Claim 9; SEQ ID NO 3168; 136pp; English.
XX	CC	Query Match Score 1503; DB 7; Length 395;		XX	PR 17-DEC-2001; 2001US-0341261P.
XX	CC	Best Local Similarity 71.8%; Score 1503; DB 7; Length 395;		XX	PA (ELITRA PHARM INC.
CC	CC	Pred. No. 6.8e-135;		XX	PI Zamudio C, Broshkin AM;
CC	CC	Sequence 395 AA;		XX	DR WPI; 2003-531017/50.
CC	CC	Query Match Score 1503; DB 7; Length 395;		XX	DR N-PSDB; ADB65041.
CC	CC	Best Local Similarity 72.9%; Score 1503; DB 7; Length 395;		XX	PT New nucleic acid, useful for preparing a composition for treating an infection caused by Cryptococcus neoformans.
CC	CC	Pred. No. 6.8e-135;		XX	PT The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence not given in the specification. A polypeptide comprising a sequence not given in the specification. A polynucleotide of the invention has fungicide activity, and may have a use in gene therapy. The nucleic acid is useful for preparing a composition for treating an infection caused by Cryptococcus neoformans.
CC	CC	Sequence 395 AA;		XX	CC The present sequence represents a C. neoformans sequence of the invention. Note: The sequence data for this patent is not represented in

the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pat_sequences.

Sequence 409 AA;

Query Match 67.9%; Score 1421.5; DB 7; Length 409;
 Best Local Similarity 69.2%; Pred. No. 4.7e-127;
 Matches 272; Conservative 51; Mismatches 67; Indels 3; Gaps 1;
 Seq 3 ARGFSKALRPMAROLATPAVORRSFVAASSMVRPATRKAAVAPTOQQTRGVKTMDFAGKKE 62
 4 SRASSNALLKALKSTASRQVARRS---SLLSGAAPRMAATLIGATCIKTDFAGKKE 60
 Db 63 QWFERADWPKKEKLLKEYFKDFTLALIGYGGQHGGQCLNLFEDNGLNUVIGTRDKGSKWDV 122
 61 VYVERADWPLDKQDQYFKNDLTLAMTGYGGQGHGSLSNARDNGLKVIVGTRKGESWIKQ 120
 Qy 123 QDGWPGKHNLFEDVDAISGTRGVINLSSDAQSETWPALKPQITKGKTLFSGHGESPVFK 182
 Db 121 EDGWPWPGGEFLDIFEPAINKGTTINLSSDAQSETWPALKPQITKGKTLFSGHGESPVFK 180
 Qy 183 DLTKEVEPFTDVDTLCAPKGSGRYTRSLFREGRINSSPAVQDTGRAEAKAIALGVAI 242
 Db 181 EDTHVTPPDKDVTDVLPAPGSGRYTRVTLLEGRIINSSIAVQDTGRAEAKAVALGIAV 240
 Qy 243 GSGLYKTTFEKEYVSDLNGERGCLMGGTHGMFLAQYEVTLRCHSPSEAFNETVEATQ 302
 Db 241 GSGLYETTFEKEYVSDLNGERGVLMGGTHGMFLAQYEVTLRKNHSPSEAFNETVEATQ 300
 Qy 303 SLYPLIGAAMDWNTEACCTTARGAIDWSPRFKDALKPQVFNOLYDSYKDGSETQRSLD 362
 Db 301 SLPPIPGKVGMDDYNNACSTTARGALDAPKKEKEANLPVFEALYNSTRDGSETRSLEF 360
 Qy 363 NSQDPRYREKYEAEETIRNLEIWRAGKAVRSLR 395
 Db 361 NSRKYTERDQKELDEIDQEIWRAGKTRVGLR 393

RESULT 15

ABU20976 ID ABU20976 standard: protein; 347 AA.
 XX AC ABU20976;
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #6503.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Bacteroides fragilis.
 XX PN W0200277183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948933.

PR 08-FEB-2002; 2002US-0342924P.

PR 06-MAR-2002; 2002US-0362693P.

XX (BLIT-) ELITRA PHARM INC.

XX Wang L, Zanudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trwick JD, Carr GJ, Yamamoto R, Forsyth RA,

DR WPI; 2003-029926/02.

N-PSDB; ACA24846.

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to
 XX isolate candidate molecules for rational drug discovery programs.

SQ Claim 25; SEQ ID NO 4890; 1766bp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC on a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 347 AA;

Query Match 52.6%; Score 1100.5; DB 6; Length 347;
 Best Local Similarity 59.9%; Pred. No. 2.3e-36;
 Matches 206; Conservative 53; Mismatches 84; Indels 1; Gaps 1;
 Qy 55 MDPAGHKEQWBRADNPKKEKLLKEYFKDFTLALIGYGGQHGGQCLNLFEDNGLNUVIGTRK 114
 4 LNFGGTENVTVTREFFPLEKAREVLLNETTAVIGYGVQGPQCSLNLRDNGFNVIG-QRP 62
 Db 115 GKSWKDAVQDGWPGKHNLFEDVDAISGTRGVINLSSDAQSETWPALKPQITKGKTLFYS 174
 63 GKTYYKAVADGTVNPGSTLFGEEAACKGTTIMCLLSDAAMSVWPTKPLTAGKLYFS 122
 Qy 175 HGFSPVPKDQLTKEVPTDVDTLCAPKGSGRYTRSLFREGRINSSPAVQDTGRAEKK 234
 Db 123 HGFATWSDR7GTVPQKDIIDVIMVAKPGSGLSLRTMFLERGLNSVAYQDATERAMER 182
 Qy 235 AIALGAIGSGSYLKYKTTPEKEVYSDLYGERGCLMGGTHGMFLAQYEVTLRERGHSPBEAFN 294
 Db 183 TIALGIGVGSGSYLKFETTFRVREATSDDLTGERSLMGAIQGLLIAQYEVLRENGHTPEAFN 242
 Qy 295 ETVEEATQSLVPLIGANGMDNNYEASSTTARGAIDWSPRFKDALKPQVFNOLYDSYKDG 354
 Db 243 ETVEEETQSLTOSMLPFAQNGMDMMYANCSSTTAORGALIWMGPFDIAIPVQLYNSVTKGN 302
 Qy 355 ETQRSIDLYNSQDYRXYEAEEMEINLNEITWRAGKAVRSLRPEN 398
 Db 303 EAQISIDSNSKEDYREKLEAKKALESEEMWQATVTRKRPEN 346

Search completed: March 22, 2006, 15:27:03
 Job time : 118.529 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	1856	88.6	400	JC1428	ketol-acid reducto
2	1503	71.8	395	1	ketol-acid reducto
3	1499.5	71.6	404	T40532	ketol-acid reducto
4	490	23.4	342	2	ketol-acid reducto
5	481	23.0	333	2	acetohydroxy acid
6	479	22.9	331	2	ketol-acid reducto
7	475	22.7	331	2	ketol-acid reducto
8	473	22.6	332	2	ketol-acid reducto
9	472	22.5	337	1	ketol-acid reducto
10	462.5	22.1	336	2	ketol-acid reducto
11	462	22.1	340	2	ketol-acid reducto
12	462.5	22.1	340	2	ketol-acid reducto
13	461	22.0	336	2	ketol-acid reducto
14	453	21.7	348	1	ketol-acid reducto
15	453.5	21.7	335	1	ketol-acid reducto
16	449	21.4	367	1	ketol-acid reducto
17	447	21.3	581	2	ketol-acid reducto
18	446	21.3	340	2	ketol-acid reducto
19	441	21.1	591	1	ketol-acid reducto
20	441	21.1	591	2	ketol-acid reducto
21	436	20.8	331	2	ketol-acid reducto
22	435	20.8	334	2	alpha-keto-beta-hydroxy acid
23	428	20.4	344	1	probable ketol-acid
24	427	20.4	363	2	ketol-acid reducto
25	427	20.4	595	1	ketol-acid reducto
26	424	20.2	337	2	ketol-acid reducto
27	424	20.2	337	2	ketol-acid reducto
28	409.5	19.6	332	2	ketol-acid reducto
29	406	19.4	333	2	ketol-acid reducto

ALIGNMENTS

RESULT 1					
JC1428	ketol-acid reductoisomerase	(EC 1.1.1.86)	- Neurospora crassa		
N;Alternate names:	alpha-keto-beta-hydroxylacyl reductoisomerase				
C;Species:	Neurospora crassa				
C;Date:	10-Sep-1999	#sequence_revision	10-Sep-1999	#text_change	05-Oct-2004
C;Accession:	JC1428				
R;Sista,	H ; Bowman, B.				
Gene 120, 115-118, 1992					
A;Title:	Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-b				
A;Reference number:	JC1428; MUID:93013010; PMID:1398116				
A;Accession:	JC1428				
A;Map position:	V				
A;Intron:	68/1; 78/3; 170/3; 392/3				
C;Superfamily:	ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase homolog				
C;Keywords:	isoleucine-valine biosynthesis; isomerase; mitochondrial; oxidoreductase				
F;87-273/Domain:	ketol-acid reductoisomerase homology <KAR>				
Query Match	88.6%	Score 1856;	DB 1;	Length 400;	
Best Local Similarity	86.8%	Pred. No. 5; 2e-134;			
Matches 349;	Conservative 35;	Mismatches 14;	Indels 4;	Gaps 2;	
Qy	1	MSARGFSTKALRMRQLATPAVORYSFVAASSNVRAT-RKAVAVPTQQIREGVTKTMDF	58		
Db	1	MAARNTCAKLRPLRQLATPAVORTYAAASAVRASYAVAKVAAPARQVQRGVTKTMDF	60		
Qy	59	GHKQWQWERADWPKKELFVKDDTLALIGYGSQGHGQGLNLRDNGLNVIIIGYRKDGKSW	118		
Db	61	GHKQEWHERADWPKKELDFTKNDTALIGYGSQGHGQGLNLRDNGLNVIGYRKDGKSW	120		
Qy	119	KDAVQDGTVPGPKNLFEDVDAISGTVMNLLSDAQSETWTALKPQTKGKTYFSGFES	178		
Db	121	EDAIQDGWVPGKNUFDVDEAISRGTVVNNLLSDAQSETWTWKPKDITKGKTYFSGFES	180		
Qy	179	PVFKDLTKVEPTDVILCAPKGSGRTVSLFREGRGINSSPAVYQDTGEAEKAVAL	238		
Db	181	PVFKDLTKVEPTDVILVAPKGSGRTVSLFREGRGINSSPAVYQDTGKAEKAVAL	240		
Qy	239	GVAIGSGLYKTTFEKEYSDLYGERGCLMGGTHGMFLAQEYVLRERGHSPSAFAFNETVE	298		
Db	241	GVAVGSGLYETFEKEYSDLYGERGCLMGGTHGMFLAQEYVLRERGHSPSAFAFNETVE	300		
Qy	299	EAQSLYPLIGANGMDWVYEAFTTARGAIDWSPRFKDALKEVNOLYDSVKDGETQR	358		
Db	301	EAQSLYPLIGANGMDWVYEAFTTARGAIDWSPRFKDALKEVNOLYDSVKDGETQR	360		
Qy	359	SLDYNSQPDYREKEAEMBEIRNLEWRAKGAVRSLRPENQK	400		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

Description

JC1428

ketol-acid reducto

ketol-acid reducto

ketol-acid reducto

acetohydroxy acid

ketol-acid reducto

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:27:29 ; Search time 21.1579 Seconds
(without alignments)

1828.118 Million cell updates/sec

Title: US-10-797-248A-1

Perfect score: 2094

Sequence: 1 MSARGFSKALRPMARQLATP.....EIWRAGKAVRSLRPPENQKQ 402

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80;*

1: PIR1;*

2: PIR2;*

3: PIR3;*

4: PIR4;*

Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ketol-acid reductoisomerase ilvc - *Bacillus subtilis*
 C;Species: *Bacillus subtilis*
 C;Accession: C69644
 C;Definition: C69644 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteletti, C.; Bron, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chodat, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, E.; Nature 390, 249-255, 1987
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerie, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hoono, S.; Hullio, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y.; M.; Ogawa, K.; Ogiwara, A.; Onega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Rieger, M.; Rivoil, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleicher, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Sezori, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*. A;Abstract: Yoshikawa, H.F.; Yamamoto, H.; Yoshikawa, H.; Danchin, A.
 A;Accession: C69644
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-342 <KUN>
 A;Cross-references: UNIPROT:P37233; UNIPARC:UPI000038DBE; GB:Z99118; GB:AL009126; NID:9
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: ilvc
 C;Superfamily: ketol-acid reductoisomerase; archaea/bacteria type; ketol-acid reductoisomerase
 F;21-202/Domain: ketol-acid reductoisomerase homology <KRP>
 Query Match 23.4%; Score 490; DB 2; Length 342;
 Best Local Similarity 36.7%; Pred. No. 8.6e-30;
 Matches 122; Conservative 68; Mismatches 118; Indels 24; Gaps 11;
 Qy 72 KEKLEIYPKDDTALLIGYGSQGHGQGIGNLRDNGVYKQGKSMKDAVQDGWVPGK 131
 Db 11 KEAVL---AGKTVAVIGTGSQGHAAHLNKESGYDVIYGVRQ-GKSFYQAOED---GK 62
 Qy 132 LFEYDEAISRGTVIMLNLSDAQSETWPA-LKEPQITKGKTLVYSHGFSPVFKDLTKVVEPV 190
 Db 63 VFSVKEAAQAEITMVLJPDQQKQVYAAEIKELDTAAKLVPAHGFVHFMQIP---P 119
 Qy 191 TDYDVILCAPKGSSRTRSLFREGGINSFAYVQDTGEAEKAAIAFGVAIG---SGYL 247
 Db 120 ADYDVLFLVAPKGCHLVLVRLTYEQAGVPAQDVTGEARDKXALAYAKTGGARAGVL 179
 Qy 248 YKTTFEKEVYSDOLYGERGCGTGHGMELAQYEVLRFGHSPSEAENFVTEATQSILYPL 307
 Db 180 -ETTEKEETEDLGEQAVLGGGSALVTKAGEFTLLEAQYQPLAYFFCLHE-LKLIVD 237
 Qy 308 IGANGMDMNYEASTTARRGAIIDMSPRFKDA-LKPVNQLYDVKQGSETRORSLDYN--S 364
 Db 238 MYEFLAGRYSISDTAQWGDPEVSGPRVYDVKYKESMEVYLDIQNTEFAKTVIENQVN 297
 Qy 365 QPDYREKEYEAEMBIRNDEIWRAGKAVRSLRP 396
 Db 298 RPRMNASENHE---QIEVYGRKLREMP 325
 RESULT 5
 F70407 acetoxyhydroxy acid isomeroeductase - *Aquifex aeolicus*
 C;Species: *Aquifex aeolicus*
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004
 C;Accession: F70407
 R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; On
 Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
 A;Reference number: A70300; MUID:9819666; PMID:9537320
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA	Qy	23.0% ;	Score 481.5 ;	DB 2 ;	Length 333 ;	
A;Residues: 1-333 <AQP>	Best Local Similarity 33.3% ;	Pred. No. 3.7e-29 ;				
A;Cross-references: UNIPROT:O67289 ; UNIPARC:UPI0000056582 ; GB:AE000730 ; NID:92983674 ; PID:916414607 ; C;Experimental source: strain VF5	Matches 110 ;	Conservative 72 ;	Mismatches 135 ;	Indels 13 ;	Gaps 6 ;	
A;Gene: ilvc						
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase <KAR>						
P;21-203/Domain: ketol-acid reductoisomerase homology						
Query Match						
Best Local Similarity						
Matches						
Qy	70	WPKKEKLLYFKDQTLALLIGYSGCGQGLNLRDNGLNTIGVKGSKWQDAVQDGWVQG 129				
Db	6	YDDEASLDLILDKVIALIGYSGCGQGLNLRDNGLNTIGVKGSKWRSREKAKADGF--- 62				
Qy	130	KNLFEVDEAISRTVIMNLLSDAAQSETWP-ALKPQITKGKTLFYSHGFSQVFKDLTKV 188				
Db	63	-EYTPTRIAAKRADIIMFLIPDTPQPEVYKNEVEPELNSSKTLAFAHGQFNHPRQIVP- 119				
Qy	189	VPTDDVQVILCAPKGSQGRVRSLSFREGCINSSPAVYQDVTGEAEEKAALGVAGS--GY 246				
Db	120	-PKDDVPEMVAPKGCPHIVRMMYTEGKCPVPAVIAHQDASGTCQDKLALAYAIGATRAG 178				
Qy	247	LYKTFTEKEVPSDPLYGERGCLMCGIHMFLAQEVLRGERHSPSEAFNETVEPATQSLYP 306				
Db	179	VIETTKEBTEDTLFGBMVLCGVTALIKAQFETLYNAGYQPEVAFBCLHL-E-LKLJLVD 237				
Qy	307	LIGANGDWWYKACSTTARRGAIDWSSPRFKDQLKPVNQLYDVSQKQSETQSLDYNSQP 366				
Db	238	LIVERGTSGMRTSISDPAKYKDVTRGERIYKVKPMEKTLTEB1QKGEFAREWILENKAG 297				
Qy	367	DYREKYEAEEMBEIRNLTEWTRAGKAVERSRRP 396				
Db	298	--RPVTTAELLERDREHLYVERKGEELRRMP 325				
RESULT 6						
AC1694						
ketol-acid reductoisomerase (acetohydroxy-acid isomero-reductase) homolog ilvc [imported]						
C;Species: <i>Listeria innocua</i>						
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004						
C;Accession: AC1694						
R;Glasser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Domanguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karet, U.						
A;Authors: Kret, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madiueno, E.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.;Rittle: Comparative Genomics of <i>Listeria</i> species.						
A;Reference number: AB1077; PMID:21537279; PMID:1679669						
A;Accession: AC1694						
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-331 <GLA>						
A;Cross-references: UNIPARC:UPI00000CC759 ; GB:AL592022 ; PID: CAC97323.1 ; PID:916414607 ; C;Experimental source: strain Clip11262						
C;Genetics:						
A;Gene: ilvc						
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase						
Query Match						
Best Local Similarity						
Matches						
Qy	78	YFKD-----DTIALIGYSGCGQGLNLRDNGLNTIGVKGSKWQDAVQDGWVQ 128				
Db	5	YFEDAYKNALEGGTKTAVIGSGQGHASHSQNLRDNGNVIIGR-BEKSAAEARNDFP-- 61				
Qy	129	GKNLFEVDEAISRTVIMNLLSDAAQSETWP-ALKPQITKGKTLFYSHGFSQVFKDLTKV 187				
Db	62	--DYYVSYSEAAKADTMILLPDETQETTYEENIKPNLKGAKVNAVPAHGFNTF--DVI 116				

118 EVPTTDVTLCAPKCSGRTRVLSPREGIRNSPFAVYQDTGEAEKALGVAIGS-G 245
 117 NPPSDVDVTLVAPKGPGHLVRRTFTEGGAVPSLAIYQDTGNARDTALSYAKGIGATRA 176
 246 YLYKTTFFKEKVVSPDLYGERGCLMGSIGHGMELAQEYVLBERGHSPEATNETVBEATQSLY 305
 177 GVIETTFFKEETETDLFGEQAVLCCGGATHLHQAGFETLVEAGYQPELAYFVEVLH-MKLIV 235
 306 PLIGANGMDWYEAQSTTARGA.DWSPRKFDALKPVNQLYDVSQDGSETOSRLSDYNS 364
 236 DQDYEYGGMKEKMRKTSNTAAYGDYVSGPRVUTADTKKAMKEVTDIQNSNFAKSFDNNK 295
 365 QPDYREKTYEAEMEEIRNLPIWRAGKAVRSIRP 396
 296 N-GPKFHRNKRQE-OQHOLEKVKAEELRNP 325

RESULT 7

31323
 31323 acetohydroxy-acid isomeroeductase (acetohydroxy-acid isomeroeductase) homolog ilvC [imported]
 Species: *Listeria monocytogenes*
 Date: 27-Nov-2001 #text_change 05-Oct-2004
 Accession: AB1323
 Glaser, P.; Franœul, L.; Buchrieser, C.; Amend, A.; Baguero, F.; Berche, P.; Bloecher, A.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madiueno, E.; Maitouram, A.; Maurel, C.; Schlueter, T.; Simoës, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.; Reference number: AB1077; MUID:21537279; PMID:11679669
 Accession: AB1323
 Status: preliminary
 Molecule type: DNA
 Residues: 1-331 <GLA>
 Cross-references: UPIPARC:UPI0000054FF8: GR:NC_003210: PTDN:CAD00064_1: PTD:G1641143.

Query Match	Score	DB 2	Length
Best Local Similarity	22.7%	Score 475;	Length 331;
	35.8%	Pred. No. 1.1e-28;	

78 XEKD-----RTIALLIGYSSOOGCGLNIRDNGINIVLISIVRKDGKSWKDAVQDGWVP 128

3 LIEDAVANNALEGKI VAVIGIGS QGHANSQNLRDNGNNVILGIR-EGRAESARNDFG--
61

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188 EVPTDVILCAPKGSGRTVRLSIREGRGINSFAVYQDVTEAAEKIALGVAIGS--G 245

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308 PLUGGING MUD MEDIUM EACHTARREAGAIDWSREFKJAD-LKPVNQLYDSVRUGSETORSLDYN
364

卷之三

296 N-GFKEFHRMRKEQ-QGHOIIEKVGAELREMP 325

אברהם ברוך רוזנשטיין: אברהם ברוך רוזנשטיין (1870-1942): אברהם ברוך רוזנשטיין (1870-1942):

Query	Match	Score	DB	Length	9
Query	Match	22.6%	Score 473; DB 2;	Length 332;	
Best Local Matches	Local Similarity	35.4%	Pred. No. 1.66-28;		
116; Conservative	Mismatches	71;	Indels	18;	Gaps
Qy	73 EKLLVEYFKDTTLALIGYSGGSGGGSGNLNRDNGLNIVIIGVRDKGSWKAQDGVWPGKNL	132			
Db	12 EVSMIDLKDVTVAWVYGNQGEAAQAKMRDLSGTVTILGIRPSSSMWRAEKGDF---	191	-EV	67	
Qy	133 FVEDEAISRGTVIMNLLSDAQSSTW-PALKPQITKGKTLFYSHGFSPVFKDLTKVEVPT	191			
Db	68 YTBEAVKRADIVHILIPDVUQPVKYREHIEPYIREGQALGFSGHFNHYKQIVP---PE	124			
Qy	192 DWDVILCAPKGSGGTVRSLSFREGGINSFAVYCDVTGEAEKAIALGVAIG--SGVLY	248			
Db	125 YVDVIMVAPKSPGPKRREKYLEGGGPVALAVYQDVTGNAKDLALAMAKAIGCTRAGVY-	183			
Qy	249 KTTPEKEVTSFLDKYERGCLMGIGHMFLAQYEVIRERGHSPFNETVEATQSLYLI	308			
Db	184 ETTFDETESDLIGEQLVYGGLIELIKKGFELVLEGPPELAYFEACNEA_KLIMDLI	242			
Qy	309 GANGMDWMMYBACSTARRGAIDWSPR-FKDALKPVENOLYDSDYRGTSETORSLDYNSQPD	367			
Db	243 YERGFTGMLKAVIDSTAKYGGLTWGPKVDDHVKENMKKAERVRSG--EFAEKWISKAD	299			
Qy	368 -YREKYEAAEMEETIRNLEIWRAGKAVRSL	394			
Db	300 KASETYEELMKPIIEEIKVGRFIRKM	327			
RESULT 9					
A96911	ketol-acid reductoisomerase [Imported]	- Clostridium acetobutylicum			
C;Species	Clostridium acetobutylicum				
C;Date	14-Sep-2001	#sequence_revision	14-Sep-2001	#text_change	05-Oct-2004
C;Accession	A96911				
R;Nolling, J.;	Breton, G.;	Oneilchenko, M.V.;	Markarova, K.S.;	Zeng, Q.;	Gibson
J. Bacteriol.	183, 4823-4838, 2001				
A;Title	Genome Sequence and Comparative Analysis of the Solvent-Producing Bacteria				
A;Reference number	A96900;	MUID:21355325;	PMTD:21355325		
A;Accession	A96911				
A;Status	preliminary				
A;Molecule type	DNA				
A;Residues	1-337 <KUR>				
A;Cross-references	UNIPROT:Q97M70; UNIPARC:UPI00000C9D5C;	GB:AE001437;	PIDN:AC		
A;Experimental source	Clostridium acetobutylicum ATCC824				
C;Genetics:					
C;Gene:	CAC0091				
C;Superfamily	ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid				
Query	Match	22.5%	Score 472; DB 2;	Length 337;	
Best Local Matches	Local Similarity	34.2%	Pred. No. 2-28;		
115; Conservative	Mismatches	65;	Indels	24;	Gaps

Qy	76 LEYFKDDTLALIIGYGSQGHGGLNLRDGLNVIIGVRKGSKWDQDGWPGKRNLLFFV 135	Db	290 ---DYGAGRPLKLTAYREQANLITEKVGAELRKAMP 322
Db	14 INYLDKCKKALIIGFSQGHAAHALNLUKEGNNVIVELYDGSKSWKAEDGF----EVYEV 69		
Qy	136 DEASIRGTTVIMNLLSDAAQSETWPA-LKPQITKGKTLFYSHGFSPVKEVLTKVEVPTDWD 194		RESULT 11
Db	70 ADAVQAAQVMILLPDEKDKOYEAESTIKONIDEGALFRAHGFTNHYQD1VPP---PKND 126		
Qy	195 VILCAPKGSGRTVSLFREGRGINSFAVYQDVTCEAEEKAIALGVAIG-SGVLKTTF 252		
Db	127 VLMIAPKGPKHIVRQYTESGGVPCLYAHQDTSKGKETALAKGKIGTKGSMNTF 186		
Qy	253 EKEVYSDLXGERGIGLGMGFLAQEVYERGRHSPSAFNETVEATQSLYLLIGANG 312		
Db	187 KIETEDLFGEQBAVQVLGGCALINAGYDIREAGYSAENAYFECFEE-NKMIIVDLYMECG 245		
Qy	313 MDNNYYEACSTTARGAIDNSPR-FKDALKPKEVNFOLYDSTYKDGSETQTSU--DYNNSQDPYR 369		
Db	246 MARYKYSISDPAEXDYVGNRLINDNRAEMKCVLTERQDTGTPAKNWLENQNGRPAFN 305		
Qy	370 EKYAEAMEEIRNLFLWRAKAVRSL---RPNQ 399		
Db	306 ARRTEADRR---E1EYKVGRKRLGMMSSWINENPSNE 337		
			Query Match 22.1%; Score 462.5; DB 2; Length 340;
			Best Local Similarity 35.4%; Pred. No. 1..1e-27;
			Matches 115; Conservative 57; Mismatches 124; Indels 29; Gaps 9;
			Qy 83 TLALIGYGSQGHGGLNLRDGLNVIIGVRKGSKWDQDGWPGKRNLLFFVDEAISRG 142
			Db 19 TVALIGYGSQGHAAQNLRDSGQEVIVGLR-PEKSWDKAEDGF---QVSYSTREAASTA 73
			Qy 143 TVMNLILSDAAQSETWPA-ALKPQITKGKTLFYSHGFSPVKEVLTKVEVPTDWDVILCAPK 201
			Db 74 DVIMLILPDEHQPTVYKNEBIEPELSEGTLAFAHGFNTVHENQ1VP---PATVDVFLAARK 130
			Qy 202 GSERTVSLFREGRGINSSFAYVQDVTGEAEKALALGVAIGSCY--LYKTTFKEKVYSD 259
			Db 131 GPGHLVRRTYDAGVPGLVAVTQDATQAKDIALYKSQNGSARAGVYETTEQETED 190
			Qy 260 LYGERGCLMGIGTHGMFLAQEVYLRERGHSPSEAFNETVEATQSLYPLIGANGMDWYEA 319
			Db 191 LFGEQAVLGCGTSALVKGAFETLVEAGQPEVAYFECIHE-LKLIVDLYMEGGLEYRYS 249
			Qy 320 CSTARRGAIIDNSPRFDA-LKEVFNQLYDYSVKDGS-----ETQRSLDYNSQPDYEBK 371
			Db 250 ISPTAQWQDFQAGPRTVTAETROAMKQILSQTGKPAKGWILENQAN-----RPE 300
			Query Match 22.1%; Score 462.5; DB 2; Length 336;
			Best Local Similarity 36.3%; Pred. No. 1..1e-27;
			Matches 122; Conservative 54; Mismatches 131; Indels 29; Gaps 10;
			Db 301 FTAINERERKHPLEVGVRELRMP 325
			Qy 76 LEYFKDDTLALIIGYGSQGHGGLNLRDGLNVIIGVRKGSKWDQDGWV 127
Db	1 MEYKDXVKVAAALDGKKGKIAVIGYGSQGHAAQNLRDGSRVGIVLGR-PEKSFDRAKEDGF- 58		RESULT 12
Qy	128 PGKNLPEVDEAISRTGTVMLNLLSDAAQSETWPA-LKPQITKGKTLFYSHGFSPVKEVLTK 186		
Db	59 ---DVTYVREATKLADVIMLAPDQIQLYEABIAPILEAGNAVGFAHGFNTFEE---F 112		
Qy	187 VEPTDWDVLLCAPKGSGTIVLREGRGINSFAYVQDVTGEAEKAI--ALGVAGS 244		
Db	113 IKVPAVDVYFMCAPKGPGHVLVRRTYEEFGCVPALAYQDATGNAKNIAAMDWCKGVAAR 172		
Qy	245 GYLYKTTPEKEVYSDLYGRGCLMGIGTHGMFLAQEVYLRERGHSPSEAFNETVEATOSL 304		
Db	173 VGLIETTYKEETEDLFGQAVLJGGJLALIBAGFEVLTGAPLAEVFLH8-NKL 231		
Qy	305 YPLJGANGMDWYEAFCSTARRGAIIDNSPR-FKDALKPENQLYDVSQKDGSETORSLDYN 363		
Db	232 VDLIYEGGGPKMRSISNTAAYGDPYVSGSRVITEQVKENMKVLAQDNGKCPANDFVN-- 289		
Qy	364 SQPDY---REKYEAEMEEIRNLFLWRAKAVRSLRP 396		

C:Genetics:

A:Gene: ilvc

C; Superfamily: ketol-acid reductoisomerase; archaea/bacteria type; ketol-acid reductoisomerase; 1somerase; oxidoreductase

Query Match Score: 22.1%; Length: 340; Best Local Similarity: 36.3%; Pred. No. 1..e-27; Matches: 122; Conservative: 54; Mismatches: 131; Indels: 29; Gaps: 10;

Qy 76 LEYFKD-----DTLALIGKSSQGHGCGLNLRDGLNVIIGVRDGKSWDAVQDGW 127

Db 5 MEYEDVKVKAALDKKIAWIGSSQGHAAQHANLRSRDRDVIIGR-PGKSFDAKEQGP- 62

Qy 128 PGKNLFEVDDEAISRGTVIMNLSSDAQSETWPA-LKPQITKGKTLFYSFGFSPVKDQTK 186

Db 63 ---DTYTVAAETKLADVIMLAPDEIQQLYAEIAAPNLEAGNAVGAFHGNLHFE---F 116

Qy 187 VEYPTDVFVILCAPKGSSRTYRSFREGINSFSAVYQDVGEAEKAI--ALGVAIGS 244

Db 117 IKVBDADYWFMCAPKGSSRTYEEGFGPGLVRLRTYEGFGPGLVPAIYQDADTNAKNTMDWCKGVGAAR 176

Qy 245 GYLXKTTPEKEVYSDLYGERGCLMGGIHMPMLQYEVLRGERGHSPEANFETVEATQLS 304

Db 177 VGLIETTYKEETEEDLPGHQAIVLGGGLTALIENGFEVLTAEYAPALEYFETLHE-MKLI 235

Qy 305 YPLIGANGDMMYEAFCSTARRGAIDWSPR-FKDALKPENQDVSYRDGSSETQRSLDYN 363

Db 236 VDLIYEGGFKEKQRQISNTAEXYGDYVSFRVITBQVKENMKAVALDIQNGKPANDFVN- 293

Qy 364 SQPYY---REKTYEAEMESTTRIETIWRACKAVRSLRP 396

Db 294 ---DYKAGRPLKAYREQANLIEKVGAEILRCAMP 326

RESULT 13

D72362 ketol-acid reductoisomerase - Thermotoga maritima (strain MS88)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004

Qy 245 GYLXKTTPEKEVYSDLYGERGCLMGGIHMPMLQYEVLRGERGHSPEANFETVEATQLS 304

Db 177 VGLIETTYKEETEEDLPGHQAIVLGGGLTALIENGFEVLTAEYAPALEYFETLHE-MKLI 235

Qy 305 YPLIGANGDMMYEAFCSTARRGAIDWSPR-FKDALKPENQDVSYRDGSSETQRSLDYN 363

Db 236 VDLIYEGGFKEKQRQISNTAEXYGDYVSFRVITBQVKENMKAVALDIQNGKPANDFVN- 293

Qy 364 SQPYY---REKTYEAEMESTTRIETIWRACKAVRSLRP 396

Db 294 ---DYKAGRPLKAYREQANLIEKVGAEILRCAMP 326

RESULT 14

F64492 ketol-acid reductoisomerase (EC 1.1.1.86) - Methanococcus jannaschii

C;Species: Methanococcus jannaschii

C;Accession: P64492

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

Qy 245 GYLXKTTPEKEVYSDLYGERGCLMGGIHMPMLQYEVLRGERGHSPEANFETVEATQLS 304

Db 177 VGLIETTYKEETEEDLPGHQAIVLGGGLTALIENGFEVLTAEYAPALEYFETLHE-MKLI 235

Qy 305 YPLIGANGDMMYEAFCSTARRGAIDWSPR-FKDALKPENQDVSYRDGSSETQRSLDYN 363

Db 236 VDLIYEGGFKEKQRQISNTAEXYGDYVSFRVITBQVKENMKAVALDIQNGKPANDFVN- 293

Qy 364 SQPYY---REKTYEAEMESTTRIETIWRACKAVRSLRP 396

Db 294 ---DYKAGRPLKAYREQANLIEKVGAEILRCAMP 326

RESULT 15

C90204 ketol-acid reductoisomerase (ilvC-1) [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Accession: C90204

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-P; Jeng, I.; Jeffries, A.C.; Koera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001
 A; Description: *Sulfolobus solfataricus* complete genome.

A; Reference number: A9139

A; Accession: C90204

A; Status: preliminary

A; Molecule Type: DNA

A; Residues: 1-35 <KUR>

A; Cross-references: UNIPROT:Q9UWX9; UNIPARC:UPI000012D50D; GB:AE006641; NID:gi13813740; F

C; Genetics:

A; Gene: ilvC-1

C; Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase; ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase

Query Match 21.7%; Score 453.5; DB 2; Length 335;
 Best Local Similarity 35.7%; Pred. No. 5.1e-27;
 Matches 111; Conservative 60; Mismatches 107; Indels 33; Gaps 9;

Qy 76 LEYFKDDTALLIGYGSQGHGQGLNLRDNGLNVIIIGVRDGKSKWDAVQDGWPCKNLFEV 135

Db 15 LDDLIKGRKIAVIGYGSQGRAWAQNLRSIGLNVVGLEREGSWELAKSDG1TP---LHT 70

Qy 136 DEAISRGTVIMNLLSDAAQSETW - PALKPQITKGKTYLFSHGFSPVFKDLTKVEVPTD 194

Db 71 KDAVKDADIIIFLVPDMVQRTLWESVQPTMKKGADLVFAHGFNTYK---LIDPPPKDSD 127

Qy 195 VILCAPKGSBTVRSLEPREGKINSSFAYQDVTEGAEEKAIALGVAIGS--GTYLKTKP 252

Db 128 VYMIAPKGPGPTVREYYKAGGGVPALVAVHODVSGTALKALATAKGIGATRAGVTPF 187

Qy 253 EKEVYSDLYGERGCLMGGTHGMELAQEVYLERGHSPSEAFNETVBEATOSLYPLIGANG 312

Db 188 KEETETDLFGBQVILGGIMELMRAFETLVEEGYQPEVAYFETINE-LKMLVDPVYERG 246

Qy 313 MDWMYEACSTARR-----AIDWS - PFKDALKPV -----FNGLYDSTK 351

Db 247 ISGMLKAVSDTAKYGGMTVGKFVIDESVCRMKEALQRKSGKFAEEWVVEYGRGMPTV 306

Qy 352 DG-SETQFSLD 361

Db 307 NGLSNVQNSLE 317

Search completed: March 22, 2006, 15:34:32
 Job time : 22.1579 sec

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Scoring table:	BIGSUM62						
Gapop	10.0 , Gapext 0.5						
Searched:	2166443 seqs, 705528306 residues						
Total number of hits satisfying chosen parameters:	2166443						
Minimum DB seq length:	0						
Maximum DB seq length:	200000000						
Post-processing:	Minimum Match 0% Maximum Match 100% Listing First 5 summaries						
Database :	UniProt 05.80: 1: uniprot_sprot: 2: uniprot_trembl: *						
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES							
Result No.	Query	Score	Match	Length	DB	ID	Description
1	2081	99.4	400	2	Q52F28	MAGGR	Q52F28 MAGGR PRELIMINARY; ID: Q52F28; PRT: 400 AA.
2	1881	89.8	402	1	ILV5_NEUCHR		AC: Q52F28; DT: 13-SEP-2005 (TREMBLrel. 31, Created)
3	1861.5	88.9	405	2	Q4HY40	GLIBBERELLA	DT: 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
4	1673	80.0	508	2	Q4WYWA	ASPPU	DT: 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
5	1581.5	79.9	400	2	Q5BAA4	EMENT	DB: Hypothetical protein.
6	1581.5	75.5	398	2	06CAFS_YARLI		GN: ORFNames:MG01808; OS: Magnaporthe grisea 70-15.
7	1542	73.6	399	2	Q6BL24	DEBRA	OS: Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaportheae; Magnaporthe.
8	1530	73.1	397	2	Q6CY71	KULJUTA	OC: NCBI_TaxID=242507; [1]
9	1526.5	72.9	400	2	Q59W5S	CANPAL	RN: NUCLEOTIDE SEQUENCE.
10	1505.5	72.8	400	2	Q59XR8	CANDIDA	RC: STRAIN=10-15;
11	1505.5	71.9	399	2	Q6FXG6	CANGA	RA: Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya B., Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S., Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A., Bayol T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L., Calvo S., Camarata B., Brunache A., Butler J., Calixte N., Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C., David R., Darrow T., Degrug S., Dooley K., Dorje P., Doreis L., Duffey N., Dupes A., Elkins T., Engels R., Erickson J., Farina A., Faro S., Ferreira P., Fischer H., Fitzgerald M., Foley J., Gage D., Galagan J., Gearin G., Gnerre S., Gniorek A., Goyette A., Graham J., Grandbois E., Gyaltset K., Hafez N., Hagopian D., Hagos B., Hall J., Hatchler B., Heller A., Higgins H., Honan T., Horn A., Houdne A., Hughes L., Hulme W., Husby E., Iliev I., Jaffe D., Jones C., Kama A., Kamyselis M., Karlsson E., Kelle C., Kleu A., Kiser P., Kodira C., Kubota B., Labutti K., Laiwa D., Landers T., Leger J., Levine S., Lewis D., Lewis T., Lindblad-ton K., Liu X., Lokytiang T., Lokytiang Y., Lucien O., Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Manning J., Marabella R., Maru K., Mattheus C., Mauceli B., McCarthy M., McDonough S., McGhee T., Meldrim J., Menus L., Mihalev A., Mihova T., Mikkelsen T., Milne V., Moru K., Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C., Nguyen N., Nguyen T., Nicoll R., Nielson C., Nizari M., Norbu C., Norbu N., O'donnell P., Okawo O., O'leary S., Omotosho B., O'neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piganani B., Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C., Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P., Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T., Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C., Spencer B., Stalker J., Stange-thomann N., Stavropoulos S., Sietzen K., Stone C., Subbs M., Talamas J., Tchuinga P., Tenzing P., Tesfaye S., Theodore J., Thoulaitang Y., Topham K., Towy S., Tsamla T., Tsomao N., Vallee D., Vassiliev H., Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T., Wangdi T., Whittaker C., Wilkison J., Wu Y., Wyman D., Yada S., Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L., Zimmer A., Zody M., Lander E.,
12	1503	71.8	395	1	ILV5 YEAST		
13	1501	71.7	395	2	Q02341	YEAST	
14	1499	71.6	404	2	ILV5_SCHPO		
15	1489	71.1	395	2	Q02340	YEAST	
16	1467.5	70.1	394	2	Q75CW4	ASHBYA	
17	1433.5	68.5	401	2	Q55QW8	ASPGO	
18	1433.5	68.5	401	2	Q5KPA9	CRANE	
19	1416.5	67.6	401	2	Q96VZ5	CRANE	
20	1253	59.8	625	2	Q4P572	USTIMA	
21	1119	53.4	352	2	Q94135	PIROMYCES	
22	1102	52.7	362	2	Q5L9J3	PIROMYCES	
23	1102	52.6	359	2	Q8A612	BACTEROIDES	
24	1100.5	52.6	347	2	Q64P71	BACTEROIDES	
25	1043	49.8	401	2	Q847RS	ASTER	
26	510.5	24.4	341	2	Q5KWJ2	GEOKYA	
27	507	24.2	341	2	Q8RL86	BACST	
28	494	23.6	332	1	ILV5 PYRFU		
29	490	23.4	342	1	P3753	PYROCOCCUS	
30	481.5	23.0	333	1	ILV5_AQUAE		
31	479	22.9	331	1	ILV5_LISTIN		

RT	"The genome sequence of <i>Magnaporthe grisea</i> .";
RT	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=70-15;
RA	Dean R., Mitchell T., Brown D., Pan H., Thon M., Thon M.;
RL	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RP	[3]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=70-15;
RA	Zhu H., Blackmon B.,
RL	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC	-1 - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC	1
DR	EMLB: AAC010001211; EA561571; -; Genomic_DNA.
DR	InterPro; IPR00006; ACh_isboundctse.
DR	InterPro; IPR009014; Transketo_C_Like.
DR	PFam; PF01450; IL1C; 1.
KW	Hypothetical protein.
SQ	SEQUENCE 400 AA: 44/23 MW: 4C8B931495B6D75 CRC64;
Query Match	99.4% Score 2031; DB 2; Length 400;
Best Local Similarity	99.8% Pred. No. 6e-141;
Matches	399; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MSARCFSKLPRMQLAPAVQYRSFVYASSMVRATAKAAVAPTOQQTGKTMDFAGH 60
Db	1 MSARCFSKLPRMQLAPAVQYRSFVYASSMVRATAKAAVAPTOQQTGKTMDFAGH 60
Qy	611 KEQWERAQWPKKEKLEYFDDTALIGTSQEHGQGLNLRDGLNTIGVRKDGSWKD 120
Db	611 KEQWERAQWPKKEKLEYFDDTALIGTSQEHGQGLNLRDGLNTIGVRKDGSWKD 120
Qy	1211 AVQDGWPGPKNLFEVDEA1 SRGTVMNLLSDAASETWALKPQTQKTLFISHGFSPV 180
Db	1211 AVQDGWPGPKNLFEVDEA1 SRGTVMNLLSDAASETWALKPQTQKTLFISHGFSPV 180
Qy	1811 FKDITKVEVPTDVILCPKGSRTVRLFREERGINSFAYQDVTGEAEKAIALGV 240
Db	1811 FKDITKVEVPTDVILCPKGSRTVRLFREERGINSFAYQDVTGEAEKAIALGV 240
Qy	2411 AIGSSYLYKTCFKEVYSLQYLYGRCCLMGGIHGMPLAQEYVLRGRHSPEAFNETVEA 300
Db	2411 AIGSSYLYKTCFKEVYSLQYLYGRCCLMGGIHGMPLAQEYVLRGRHSPEAFNETVEA 300
Qy	3011 TQSLYPLIGANGMDMYEACSTTARGADWSRPFKDAKLPVNQLYDSVQGSETQL 360
Db	3011 TQSLYPLIGANGMDMYEACSTTARGADWSRPFKDAKLPVNQLYDSVQGSETQL 360
Qy	3611 DYNSPDYREKYEAEEMEEIRNLIEWRAGRAVSRPENQK 400
Db	3611 DYNSPDYREKYEAEEMEEIRNLIEWRAGRAVSRPENQK 400
RESULT 2	
ID	ILV5_NEUR STANDARD;
AC	P38774; Q7RVDS; Q8A019;
DT	01-FEB-1995 (Rel. 31, Created)
DT	10-OCT-2003 (Rel. 42, Last sequence update)
DT	13-SEP-2005 (Rel. 48, Last annotation update)
DE	Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86) (Aceto-hydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylaci
DE	reductoisomerase).
DE	Name=ilv-2; ORFNames=B1LH24_150, NCU03608;
OS	Neurospora crassa
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC	Sordariaceae; Sordariaceae; Neurospora.
[1]	NCBI_TaxID=5141;
RN	NUCLEOTIDE SEQUENCE.

DE	reductoisomerase;
DS	ORENames=FG10118;1.
DS	Gibberella zeae PF-1.
DC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
DC	Hypoconiothyceidae; Hypocreales; Nectriaceae; Gibberellaceae;
NCBI_TAXID	229533;
DN	[1]
DN	NUCLEOTIDE SEQUENCE.
SP	STRAIN=PH-1;
RC	NUCLEOTIDE SEQUENCE.
RA	Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L., Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J., Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K., Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R., Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J., Gardyna S., Gnevre S., Graham L., Grand-Pierre N., Hafez N., Hagopian D., Hago S., Hall J., Horton L., Hulme W., Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Karatas A., Kellis C., Landers J., Levine R., Lindblad-Toh K., Liu G., Lui A., Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J., Matthews C., Maucler E., McCarthy M., Meldrum J., Menuez L., Mihoa T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S., Rachupka A., Ranasamy U., Raymond C., Retta R., Rise C., Rogov P., Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smitrov S., Smith C., Spencer B., Strange-Thomann N., Stojanovic N., Stubbs M., Talamas J., Testayre S., Theodore J., Topham K., Travers M., Vassiliiev H., Venkataraman V., Viel R., Vo A., Wang S., Wilson B., Wu X., Wyman D., Young G., Zainoun J., Zody M., Zimmer A., Zembek L.,
RA	"Fusarium graminearum genome sequence";
RA	"Fusarium graminearum genome sequence";

RX	PubMed:15229592; DOI:10.1038/nature02579;	OX	NCBI_TaxID=4959;
RA	Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marcq C., Neuveglise C., Talla E., Goffard N., Frangoul L., Aigle M., Anthouard V., Babbé V., Baray S., Blanchin S., Beckrich J.-M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confaniolieri P., de Daruvar A., Desprons L., Fabre E., Fairhead C., Ferry-Dumaset H., Groppi A., Hantreay F., Henneguin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Kozsul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A., Swannen D., Tekala F., Wesołowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincher P., Souciet J.-L.,	RN	[1] Nucleotide sequence [LARGE SCALE GENOMIC DNA].
RT	"Genome evolution in yeasts".	RP	
RL	Nature 430:35-44 (2004); EMBL; CR382130; CAGB0542.1; "Genomic DNA."	RC	STRAIN=ATCC 36239 / CBS 6767;
DR	GO:0004455; P:retol-acid reductoisomerase activity; IEA.	RX	PubMed=15229592; DOI=10.1038/nature02579;
DR	GO:0016491; P:oxidoreductase activity; IEA.	RA	Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marcq C., Neuveglise C., Talla E., Goffard N., Frangoul L., Aigle M., Anthouard V., Beyne E., Bleykasten C., Baray S., Blanchin S., Beckrich J.-M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confaniolieri P., de Daruvar A., Desprons L., Fabre E., Fairhead C., Ferry-Dumaset H., Groppi A., Hantreay F., Henneguin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Kozsul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A., Swannen D., Tekala F., Wesołowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincher P., Souciet J.-L.,
DR	InterPro: IPR00006; AchI_isomrdctse.	RA	"Genome evolution in yeasts.".
DR	PF01450; ilvc; 1.	RT	Nature 40:35-44 (2004); EMBL; CR382138; CAGB0542.1; "Genomic DNA."
DR	PF01450; ilvc; 1.	DR	GO:0016853; P:isomerase activity; IEA.
DR	TIGRFAMS; TIGR00465; ilvc; 1.	DR	GO:0004455; P:ketol-acid reductoisomerase activity; IEA.
KW	Complete proteome.	DR	GO:0009052; P:branched chain family amino acid biosynthesis; IEA.
SEQUENCE	398 AA; 44160 MW; C98CB7C8AFE26F1 CRC64;	DR	InterPro: IPR00006; AchI_isomrdctse.
Query Match	1 MSARGFSKALRPMAQOLATPAVQVRSFVAASSMVF-RATVKAAYAAPTQQIQRGVKTMDF58	DR	PFam; PF01450; ilvc; 1.
Best Local Similarity	75.5%; Score 158.5%; DB 2; Length 398;	DR	TIGRFAMS; TIGR00465; ilvc; 1.
Matches	304; Conservative 44; Mismatches 46; Indels 7; Gaps 3;	KW	Complete proteome; Isomerase; Sequence 399 AA; 44352 MW;
Qy	1 MSARLFISTA---SQAARRAVARYATVSAARSRSIAMAATPAAFLSAPAVARTKTTNS 56	DR	53D67F203BD09113 CRC64;
Db	1 MSARLFISTA---SQAARRAVARYATVSAARSRSIAMAATPAAFLSAPAVARTKTTNS 56	DR	5D67F203BD09113 CRC64;
Qy	59 GHKEQ-VWERADWPKEPKLLEYFQDTLALIGYGSQHGGQCLNLNDGGLAVIIGVRDGKS 117	DR	53D67F203BD09113 CRC64;
Db	57 GKEDELVHERADWPQEKLLDYFQNDTIALIGYGSQHGGQCLNLNDGGLAVIIGVRDGKS 116	DR	53D67F203BD09113 CRC64;
Qy	118 WKDAVQDGWYFGKNUFEDVIAISRGTVIINILSDAQSETWPAKRPQTGKTLYFSGKF 177	DR	53D67F203BD09113 CRC64;
Db	117 WKAQDGWYFGKNUFEDVIAISRGTVIINILSDAQSETWPAKRPQTGKTLYFSGKF 176	DR	53D67F203BD09113 CRC64;
Qy	178 SPVFKDLTKYEVPTDVLILCAPKGSGRTVSLFREGCINSSFAVYQDVTGEAREKAYA 237	DR	53D67F203BD09113 CRC64;
Db	177 SPVFKDLTKYEVPTDVLILCAPKGSGRTVSLFREGCINSSFAVYQDVTGEAREKAYA 236	DR	53D67F203BD09113 CRC64;
Qy	238 LGVATGSGGLYKTTFEKEVTSDFLYGERGLCLMGGIHGMFLAQEVYLRERGHSPAFNETV 297	DR	53D67F203BD09113 CRC64;
Db	237 LAIATGSGGYVQTTFEKEVSDLYGERGLCLMGGIHGMFLAQEVYLRERGHSPAFNETV 296	DR	53D67F203BD09113 CRC64;
Qy	298 BEATQLYPLIGANGIDMWYACSTTARGAIDNSPRFDKALKEPVFNQYDSDVYKDGSETQ 357	DR	53D67F203BD09113 CRC64;
Db	297 BEATQLYPLIGANGIDMWYACSTTARGAIDNSPRFDKALKEPVFNQYDSDVYKDGSETQ 356	DR	53D67F203BD09113 CRC64;
Qy	358 RSLDYNNSQDPYREKYEAMEMBIRNLIRWAGKAVSLRPEN 398	DR	53D67F203BD09113 CRC64;
Db	357 RSLEFNNSQDYZKFAELQDIRLIEWVYKEVRKLRPEN 397	DR	53D67F203BD09113 CRC64;
RESULT 7	Q6BLZ4 -DEBHA PRELIMINARY;	DR	53D67F203BD09113 CRC64;
ID	Q6BLZ4 -DEBHA PRELIMINARY;	PRT	399 AA.
AC	Q6BLZ4	RESULT 8	
DT	25-OCT-2004 (TREMBrel. 28, Created)	Q6CY71 KLULA	
DT	25-OCT-2004 (TREMBrel. 28, Last sequence update)	ID	
DT	25-OCT-2004 (TREMBrel. 28, Last annotation update)	AC	Q6CY71
DE	Similar to cal1CA1981 CaliV5 Candida albicans CaliV5 ketol-acid reducto-isomerase.	DT	25-OCT-2004 (TREMBrel. 28, Last sequence update)
GN	OrderedLocusNames=DNA00F10483G;	DT	25-OCT-2004 (TREMBrel. 28, Last annotation update)
OS	Debaryomyces hansenii (Yeast) (Torulomyces hansenii)	DE	Kluyveromyces lactis strain NRRL Y-1140 Chromosome A of strain NRRL Y-
OC	Fungi; Ascomycota; Saccharomycetaceae; Debaryomyces;	DE	1140 of Kluyveromyces lactis.

GN	OrderedLocusName=KU11A026739;	DT	10-MAY-2005 (TREMBLrel. 30, Last sequence update)
OS	Kluveromyces lactis (Yeast).	DT	10-MAY-2005 (TREMBLrel. 30, Last annotation update)
OC	Fungi; Ascomycota; Saccharomycotina; Kluyveromycetes;	DE	Likely mitochondrial ketol-acid reductoisomerase.
OC	Saccharomycetales; Saccharomycetaceae; Kluyveromycetes.	GN	Name=ILV5; ORFNames=Co19.7733;
OX		OS	Candida albicans SC53.4.
		OC	Saccharomycetales; mitosporic Saccharomycetales; Candida.
[1]		NCBI_TaxID=437561;	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	OX	
RC	STRAIN=CS 2359 / IFO 1267 / NRRL Y-1140 / WM37;	RN	
Pubmed=152952; DOI=10.1038/nature02519;		RP	NUCLEOTIDE SEQUENCE.
RA	Dufour B., Sherman G., Durrens P., Casaregola S.,	RC	STRAIN=SC53.4;
RA	Lafontaine I., de Montigny J., March C., Neuveglise C., Taïla B.,	RX	PUBMED=15122810; DOI=10.1073/pnas.0401648101;
RA	Goffard N., Frangoulis L., Aigle M., Anthouard V., Babot A., Barbe V.,	RA	Jones T., Federerup N.A., Chibana H., Kalman S., Kalman J., Dungan J., Thorstenson Y.R., Agabian N., Magee P.T.,
RA	Barnay S., Blanchin S., Becherich J.-M., Beyne E., Bleylevstsen C.,	RA	Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA	Boizrame A., Boyer J., Cattolico L., Conflanieri P., de Daruvar A.,	RA	Davis R.W., Scherer S.;
RA	Despax L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropis A.,	PT	"The diploid genome sequence of <i>Candida albicans</i> ."
RA	Hantreux F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,	RL	Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
RA	Kerrest A., Koszul R., Lemaire M., Lescot I., Ma L., Muller H.,	[2]	
RA	Nicaud J.-M., Oztas S., Ozier-Kalogeropoulos O.,	RN	
RA	Pelizzetti S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,	RP	NUCLEOTIDE SEQUENCE.
RA	Swennen D., Tekala P., Wesołowski-Louvel M., Westhof E., Wirth B.,	RC	STRAIN=SC53.14;
RA	Zenner M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,	RA	Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA	Bouchier C., Caudron B., Scarpelli C., Gaillard C., Weissbach J.,	RA	Roberts J., Persson K., Donnelly S., Favreto S., Tzung K.-W.,
RA	Wincker P., Souillet J.-L.,	RA	Jones T., Scherer S., Agabian N.;
RL	"Genome evolution in yeasts."	RT	"Annotation of the Genome of <i>Candida albicans</i> ".
DR	EMBL; CH02121; CH02706.1; -; Genomic_DNA.	RL	Submitted (APR 2004) to the EMBL/GenBank/DBJ databases.
DR	GO:0004455; Fatty acid reductoisomerase activity; IEA.	CC	-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DR	GO:0016494; Foxidoreductase activity; IEA.	CC	DR EMBL; AACQ0100112; EAK94923.1; -; Genomic_DNA.
DR	InterPro; IPR000582; P-branched chain family amino acid biosynthesis; IEA.	KW	DR EMBL; AACQ0100112; EAK94923.1; -; Genomic_DNA.
DR	InterPro; IPR000506; Ach_ibomrdctse.	SQ	SEQUENCE 400 AA; 44848 MW; ACD3162D05078B1 CRC64;
DR	Pfam; PF01450; IIC7C; 1; IIC7C; 1.		
DR	TIGRFAMS; TIGR00465; ilvC; 1.		
KW	Complete genome.		Query Match 72.9%; Score 1526.5; DB 2; Length 400;
SQ	SEQUENCE 397 AA; 44189 MW; 7634BEC037ABA9B CRC64;		Best Local Similarity 73.8%; Pred. No. 3 8e-101; Mismatches 53; Indels 3; Gaps 3;
		Qy	1 MSARGFSKALRPMQLATPAVORRSEVA-ASSMVRATKAAVAPTO-QQIRGVKTMDFA
		Db	1 1 NSFRTSMRMRLATATAKLSKRTFSLLANATRTAAKSAAKMPITSRGVKTMDFG 58
		Qy	59 GHKEQWFERADWPKERKLEYFKDDTALIGVSGQHGLQGLNLRDNGLNVIIGVRKQKSW 118
		Db	61 GTEEVVHFERADWPKERKLEYFKDNTFALIGVSGQHGLQGLNLRDNGLNVIIGVRK-GSSW 119
		Qy	119 KDAVQDWPVGPGRNLFFVDEAISRGTVTMNLSDAASETWPALKPQITKGKTLYFSGHGS 178
		Db	120 EAEVEDGWVPGENLFLFVDEAISRGTVIMDLISDAASETWPALKPQITKGKTLYFSGHGS 179
		Qy	239 GVAIGSGYLYKTTFEKEVYSDLYGCLMGIGIHMGLAQEVYLRLRGHSSSEAFNETVE 298
		Db	240 AIAIGGSXVKTTEREVNSDLYGRCCLMGICHGFLAQEVYLRLRGHSSSEAFNETVE 299
		Qy	299 EATQSLYPLIGANGMIDMYEACSTTARGALDWSPFKDALKPVFNQLYDSVKDGSSTQR 358
		Db	300 EATQSLYPLIGANGMIDMYEACSTTARGALDWSPFKDALKPVFNQLYDSVKDGSSTQR 359
		Qy	359 SLIDYNQSPDREKYEAEEMEEIRNLIEWRAGKAVRSLRPENQ 399
		Db	360 SLBFSNRSRSDYKERLEELQITRNMEIWRVGKEVRKLRPENQ 400
			RESULT 10
			Q59XR8 CANAL
			ID Q59XR8_CANAL PRELIMINARY;
			AC Q59XR8;
			DT 10-MAY-2005 (TREMBLrel. 30, Created)
			DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
			DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
			DE Likely mitochondrial ketol-acid reductoisomerase.
RESULT 9	Q59WW5_CANAL		
Q59WW5_CANAL PRELIMINARY;	PRT;	400 AA.	
AC Q59WW5;			
DT 10-MAY-2005 (TREMBLrel. 30, Created)			

Name=ILV5; ORFNames=Ca019.8;
 OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OX Saccharomycetales; mitosporic Saccharomycetales; Candida.
 RN NCBI_TaxID=237561;
 RN [1] NUCLEOTIDE SEQUENCE.
 STRAIN=SC5314;
 PubMed=15123810; DOI=10.1073/pnas.0401648101;
 Jones T., Federici N.A., Chibana H., Dungan J., Kalman S.,' Dungan J.,
 Magee P.T., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
 Davis R.W., Scherer S.;
 RT "Annotation of the Genome of *Candida albicans*";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
 RN [2] NUCLEOTIDE SEQUENCE.
 STRAIN=SC5314;
 Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
 Roberts J., Person K., Donnelly S., Favoreto S., Tzung K.-W.,
 Jones T., Scherer S., Agabian N.;
 RT "Annotation of the Genome of *Candida albicans*";
 Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/CenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL: AAC001000106; EAK095225.1; -; Genomic_DNA.
 KW Isomerase.
 SQ SEQUENCE 400 AA; 44882 MW; FC79162D0507D8C CRC64;
 Query Match 72.8%; Score 1524.5; DB 2; Length 400;
 Best Local Similarity 73.8%; Pred. No. 5.3e-101;
 Matches 296; Conservative 48; Nsmatches 54; Indels 3; Gaps 3; .
 Qy 1 MSARGPSKCARPMARQALATAKATLSKRTSLLNATAATRYAAKAMTPISRGKTTING 58
 Db 1 MSFRTSMMRMRARLATAKATLSKRTSLLNATAATRYAAKAMTPISRGKTTING 58
 Qy 59 GHKEQWERAADWPKERKELAYFKDFTLALICGSGCGHGOGLNLRDGLTIGVRDKGSW 118
 Db 61 GTEEVVHERRADWPKERKELIDFRNDTPFALICGSGCGHGOGLNLRDGLTIGVRK-GSW 119
 Qy 119 KDAVQDGWPKGKNLFEVDEAISRGTVIMNLSDAQSETMPALKPQITGKTLPSHGS 178
 Db 120 EAEDGWWPKGENLFEVDEAISRGTVIMNLSDAQSETWFKPQITGKTLPSHGS 179
 Qy 179 PFKDQLTRKEPTDVLAKPSGKTRTSLFEGRGINSFAYVQDITGEAEAKAL 238
 Db 180 PFKDQLTRHEPPSNIDVLLAAPKGSQRTTSLFEGRGINSFAYVNDTIGKAEAKAM 239
 Qy 239 GVAIGSGLYKTTFEKEYSDLYGERGCMGGTIRHMFLAQEVYLERGHSPFAFNETVB 298
 Db 240 AIAIGSGYVKTTEKEYSDLYGERGCMGGTIRHMFLAQEVYLERGHSPFAFNETVB 299
 Qy 299 EATQSLYPLIGANGMDWMMTACSTARRGAIDWSPREKDALPKVFNQYDSVKDSETQR 358
 ..-.. 300 EATQSLYPLIGANGMDWMMTACSTARRGAIDWSPREKDALPKVFNQYDSVKDSETQR 359
 Qy 359 SLDYNSQDPRKREYKDAEMMTRNLEIWRAGKAVSLRPNQ 399
 Db 360 SLEENRSRSDYKERLBEFQFIRNMBIWRVKEVRKLRPNQ 400
 Q6FAG6 CANGA CANGA PRELIMINARY; PRT; 399 AA.
 AC Q6FAG6;
 DT 05-JUL-2004 (TREMBurrel. 27, Created)
 DT 05-JUL-2004 (TREMBurrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBurrel. 27, Last annotation update)
 DE Candida glabrata CBS138 chromosome B complete sequence.
 DN OrderLocusName=CaGL01030479;
 Candida glabrata (Yeast) (Torulopsis glabrata)
 OS Eukaryota; Fungi; Ascomycota; Saccharomycetes;
 RESULT 11

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 RN NCBI_TaxID=5478;
 RN [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 STRAIN=ATCC 2001 / CBS 138;
 PubMed=15229502; DOI=10.1038/nature02579;
 RA Dufour B., Sherman D., Fischer G., Durrens P., Casaregola S., Talla E.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Baray S., Blanchin S., Bleykasten C., Beyne E., Breyne E.,
 RA Boisrame A., Boyer J., Catelloco L., Confaniolieri F., de Daruvar A.,
 RA Despous L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennquin P., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lescure I., Ma L., Muller H.,
 RA Nicoud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Strub P., Suleau A.,
 RA Swennen D., Tekaya F., Wesolowski-Louvel M., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Boucher C., Audron C., Scarpeilli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souillet J.-L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44 (2004);
 DR EMBL: CR380948; CAG58005.1; -; Genomic_DNA.
 DR GO:0004455; F:ketol-acid reductoisomerase activity; IBA.
 DR GO:0016431; F:oxidoreductase activity; IBA.
 DR GO:0009082; P:branched chain amino acid biosynthesis; IBA.
 DR InterPro: IPR005056; AcH_isomrdctse.
 DR Pfam: PF01450; IlvC; 1.
 DR TIGRFAMS; TIGR00465; ilvC; 1.
 KW Complete proteome; 40; Mismatches 49; Indels 7; Gaps 2;
 SQ SEQUENCE 399 AA; 44568 MW; E2241C86A034D728 CRC64;
 Query Match 71.9%; Score 1505.5; DB 2; Length 399;
 Best Local Similarity 74.9%; Pred. No. 1.2e-99;
 Matches 287; Conservative 40; Mismatches 49; Indels 7; Gaps 2;
 Qy 17 LATPAVQRFSFVASMYTRATRAAAVAPTAQ-DOIGRTKMDA 76
 Db 24 LAARAASRNP--AASLMAQSKRIPVA---TRGIQINFGTVTETYERADWPREKUL 76
 Qy 77 EYFKDITLALIGYSGQHGOGLNLRDGLTIGVKTGKSNKDAVQDGWPGKRNLFVVD 136
 Db 77 NYPANTPFLIGYSGQHGOGLNLRDGLTIGVKTGKSNKDAVQDGWPGKRNLFVVD 136
 Qy 137 EAISRGTVIMNLSDAQSETWPALKPQITGKTLYFSGFSPVFKOLTKEVPTDVFV 196
 Db 137 EAVKKGTVYVNNLSDAAQSETWNNSLPKLTGKTLYFSGFSPVFKOLTKEVPTDVFV 196
 Qy 197 LCAPKGSRTVRSLSFREGRGSFAYVQDITGEAEAKALGVAIGSGLYKTTFEKEV 256
 Db 197 LVAEKGSGRTVRSLSFREGRGSFAYVQDITGEAEAKALGVAIGSGLYKTTFEKEV 256
 Qy 257 YSDIYGERGCLMGGIHMFLAQEVYLERGHSPSEAENETVETQSLYPLIGANGMDWM 316
 Db 257 NSDIYGERGCLMGGIHMFLAQEVYLERGHSPSEAENETVETQSLYPLIGANGMDWM 316
 Qy 317 YEACSTTARRGAIDWSPREKDALPKVFNQYDSVKDSETQRSDYNSQDPRKYELEM 376
 Db 317 YDACSTTARRGAIDWSPREKDALPKVFNQYDSVKDSETQRSDYNSQDPRKYELEM 376
 Qy 377 EETRNLEIWRAGKAVSLRPNQ 399
 Db 377 QTRDMEIWRVKEVRKLRPNQ 399

RESULT 12
 ILV5 YEAST STANDARD; PRT; 395 AA.
 ID ILV5 YEAST
 AC P0168;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)

DE (Aceto)hydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxyalacil reductoisomerase).	DR Ensembl: YLR355C; Saccharomyces cerevisiae.
GN Name=ILV5; Order=locusName=YLIR355C; ORFNames=IL9638 .7;	DR SGD; S000004347; ILV5.
OS Saccharomyces cerevisiae (Baker's yeast).	DR GO; GO:0426455; C:mitochondrial nucleoid; IDA.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces;	DR GO; GO:0005739; C:mitochondrion; IDA.
OC Saccharomycetales; Saccharomyctaceae; Saccharomyces.	DR GO; GO:0004455; P:ketol-acid reductoisomerase activity; TAS.
OX NCBI_TaxID=4932;	DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; TAS.
RN [1]	DR GO; GO:0000002; P:mitochondrial genome maintenance; IMP.
RP NUCLEOTIDE SEQUENCE.	DR InterPro; IPR000506; AchI_isomrdtse.
RX MEDLINE=87117524; PubMed=3027658;	DR Pfam; PF01450; ILVC; 1.
RA Petersen J.G.L., Holmberg S.;	DR TIGRFAMs; TIGR00465; ilvc; 1.
RT "The ILV5 gene of <i>Saccharomyces cerevisiae</i> is highly expressed.";	KW Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;
RL Nucleic Acids Res. 14: 9631-9651 (1986).	KW Complete proteome; Direct protein sequencing; Magnesium;
RN [2]	KW Mitochondrion; NADP; Oxidoreductase; Transit Peptide.
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	KW Mitochondrion (Potential).
RC STRAIN=S288C / AB972;	FT TRANSIT 1 47 Ketol-acid reductoisomerase.
RX MEDLINE=973112867; PubMed=9169871;	FT CHAIN 48 NADP (Potential).
RA Johnston M., Hillier L.W., Riles L., Albermann K., Andre B.,	FT NP BIND 84 NADP (Potential).
RA Ansborg W., Benes V., Bruehl H., Dubois B.,	FT REGION 363 395 Hydrophilic.
RA Duesterhoeft A., Eritian K.-D., Floeth M., Goffeau A., Kleine K.,	FT ACT SITE 171 171 Potential.
RA Heumann K., Heuss-Neitzel D., Hilbert H., Hilger P., Kleine K.,	FT SEQUENCE 395 AA; 44368 MW; D76419A6AD68E85E CRC64;
RA Koettner P., Louis H.-W., Messing F., Miosga T.,	Query Match 71.8%; Score 1503; DB 1; Length 395;
RA Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E.,	Best Local Similarity 72.9%; Pred. No. 1.8e-99;
RA Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M.,	Matches 288; Conservative 45; Mismatches 56; Indels 6; Gaps 3;
RA Rinke M., Rose M., Schafmeier B., Schoniger P., Schwäger C.,	QY 10 LRPMPQL--ATPAVORRSFAVASSMVNRATKAA--VAPTOQOIRGKVKTMDAGHKBQV 64
RA Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenberg M.,	2 LRTQARLICNSRVITAKRTFALATRAAAYSRPDAAREVFKP-MITRSLIKQINFGGTVBTV 60
RA Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H.,	QY 65 WERADWPKEKLLYEYKDDTLALIGYSSQGHGQGLNLRDNGLNIVIGYRKDGKSWKDAVQD 124
RA Wahbaut R., Wedler B., Wedler H., Zimmermann F.K., Zöllner A.,	Db 61 YERADWPKEKLLYEYKDDTFALIGYSSQGYGQGLNLRDNGLNIVIGYRKDGASWKAIED 120
RA Hani J., Hoheisel J.D.;	QY 125 GWPGRQKLFEDBAISGTVMLLSDAQSETWPALKPQITKGKTLYFSGHSPFPFKDL 184
RT "The nucleotide sequence of <i>Saccharomyces cerevisiae</i> chromosome XII.";	Db 121 GWPGRQKLFEDBAISGTVMLLSDAQSETWPALKPQITKGKTLYFSGHSPFPFKDL 180
RL Nature 387:87-90 (1997).	QY 185 TKVEVPTDVTILCAPKGSGRTVRLSFRGREGINSFSAVYQDVTGEAEKAIALGVAIGS 244
RN [3]	Db 181 THYTPKQDVTILVAPKGSGRTVRLSFRGREGINSFSAVWNDVTGKAHEKAQALAVAIIGS 240
RP PROTEIN SEQUENCE OF 166-174.	QY 245 GYLYKTFKEVKEYSDLIGERGCLMGGMQTYEVTLRERGHSPSEAQNTEVETQSL 304
RC STRAIN=S288C;	Db 241 GRYVQTFEREVNSDLYGERGCLMGGMQTYEVTLRERGHSPSEAQNTEVETQSL 300
RX MEDLINE=95203288; PubMed=7895733;	QY 305 YPLIGANGMDMIVTEAFTTARGAIDMSPRKDALKPVFNOLOYDSKDGSETORSLDYNS 364
RA Garrels J.I., Futterer B., Kobayashi R., Latter G.I., Schwender B.,	Db 301 YPLIGKYGMDDMYDAGCTTARGALWPKYTPKNAKLPVFDOLYESTKNGTETKRSJEFNS 360
RA Volpe T., Warner J.R., McLaughlin C.S.;	QY 365 QDPRYKYEAEHEINLLEIRVAKRSLSRPEQ 399
RT "Protein identifications for a <i>Saccharomyces cerevisiae</i> protein database.";	Db 361 QDPRYKKELEKDTIIMMEIWKVKEVTRKLPEQ 395
RT	RESULT 13
RN	ID Q02341_YEAST PRELIMINARY;
RP IDENTIFICATION OF PROBABLE N-TERMINUS	AC Q02341_1 YEAST PRELIMINARY;
RP MEDLINE=97121404; PubMed=89970; DOI=10.1073/pnas.93.25.14440;	AC Q02341_1 YEAST PRELIMINARY;
RA Shevchenko A., Jensen O.N., Podtelejnikov A.V., Saggiocco F., Wilm M.,	DT 01-NOV-1996 (TRMBLrel. 01, Created)
RA Vorm O., Mortensen P., Shevchenko A., Boucherie H., Mann M.;	DT 01-OCT-2003 (TRMBLrel. 01, Last sequence update)
RT Linking genome and proteome by mass spectrometry: large-scale identification of yeast proteins from two dimensional gel.";	DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
RT Proc. Natl. Acad. Sci. U.S.A. 93:14440-14445 (1996).	DE Acetylhydroxy-acid isomero-reductase.
RL C-1 CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+)	GN Name=ILV5; Synonyms=ILV5;
CC = (S)-2-hydroxy-2-methyl-1,3-dihydroxy-3-methylbutanoate + NADPH.	OS Saccharomyces cerevisiae (Baker's yeast).
CC -1 CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate + NADP(+)	OC Saccharomyces; Fungi; Ascomycota; Saccharomyctaceae; Saccharomyces.
CC -1 COFACTOR: Magnesium.	OC [1]
CC -1 PATHWAY: Aminoc-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate: step 2.	OX NCBITaxID=4932;
CC -1 PATHWAY: Aminoc-acid biosynthesis; L-valine biosynthesis; L-valine from pyruvate: step 2.	OX NCBITaxID=4932;
CC -1 SUBCELLULAR LOCATION: Mitochondrial.	RN
CC -1 SIMILARITY: Belongs to the ketol-acid reductoisomerase family.	RP NUCLEOTIDE SEQUENCE.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	RX MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925;
CC	RA Xie Q.; Jimenez A.;
CC "Cloning and molecular analysis of two different ILV5 genes from a brewing strain of <i>Saccharomyces cerevisiae</i> .";	RT Curr. Genet. 26:398-402 (1994).
CC	RL
DR X04969; CAA28643.1; -; Genomic_DNA.	DR X04969; CAA28643.1; -; Genomic_DNA.
DR U019102; AAB7753.1; -; Genomic_DNA.	DR A24709; A24709.
DR RSP; Q01292; 1QMC.	DR RSP; Q01292; 1QMC.
DR IntAct; P06168; -.	DR GermOnline; 142419; -.
DR GermOnline; P06168; -.	DR SWISS-2DPAGE; P06168; YEAST.

Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S., Skellon J., Simmonds M.N., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels B., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Duesterhoeft A., Fricke C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedlter H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dresno S., Gloux S., Lelauve V., Mortier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.I., Moreno S., Armstrong J., Forssburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Usery D., Barrel B.G., Nurse P., "The genome sequence of <i>Schizosaccharomyces pombe</i> .", Nature 415:871-880 (2002).	[2]	RN
		RP
		NUCLEOTIDE SEQUENCE [LARGE SCALE RNA].
		RC
		MDLINE=9816-2722; PubMed=9501991;
		Yoshioka S., Kato K., Okayama H., Nojima H.; "Identification of open reading frames in <i>Schizosaccharomyces pombe</i> cDNA.", DNA Res. 4:363-369 (1997).
		RL
		NUCLEOTIDE SEQUENCE OF 262-404.
		RA
		Kawanukai M.; Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
		RL
		-- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP (+) = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
		CC
		-- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate + NADP (+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.
		CC
		-- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate; step 2.
		CC
		-- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine from pyruvate; step 2.
		CC
		-- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
		CC
		-- SIMILARITY: Belongs to the ketol-acid reductose family.
		CC
		-- This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is removed.
		CC
		-- EMBL: AL023288; CAA18891.1; -; Genomic_DNA.
		DR
		-- DR: D89175; BA013837.1; -; mRNA.
		DR
		-- DR: AB009610; BA240001.1; -; mRNA.
		PIR: T40532; T40532.
		HSSP: Q9HVA2; INPS3.
		DR
		-- Genedb_Spombe; SPBC56F2.12; -.
		DR
		-- InterPro: IPR000506; Ach_isomrdctse.
		PFAM: PF01450; I1vc; 1.
		DR
		-- TIGRFAMS: TIGR00465; I1vc; 1.
		KW
		-- Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;
		KW
		-- Complete Proteome; Mitochondrion; NADP; Oxidoreductase;
		KW
		-- Transit peptide.
		TRANSIT 1
		-- CHAIN 1
		-- CHAIN 2
		-- ACT SITE 178
		-- CONFLICT 38
		-- CONFLICT 92
		-- CONFLICT 275
		-- CONFLICT 297
		-- CONFLICT 394
		-- SEQUENCE 404 AA;
		-- 45189 MW;
		-- 91AB367471AD6FB CRC64;
		Mitochondrion (Potential)
		Potential
		Potential
		S -> R (in Ref. 2).
		S -> S (in Ref. 2).
		N -> P (in Ref. 2).
		N -> P (in Ref. 2).
		V -> G (in Ref. 2).
		Score 1499.5; DB 1; Length 404;
		Best local similarity 71.1%; Pred. No. 3.3e-99;
		Matches 286; Conservative 56; Mismatches 53; Indels 7; Gaps
		2 SARGFSKALRPM-ARQLAT-PAVWRSFVAASQMVTRAEKAAPVQQQIRGVKTMDFDA

Db	6	SSRMKAKLRTMGSRLATRSMYRART-IAAPSRRFAPRMTA---PLMOTRGHRYMDEA	Qy	185 TKVEVPTDVVILCAPKGSGRTVRSLSPREGRGINSPPAVYQDVTGEABEKAIAGVAIGS
Qy	59	GHKEQWERADWPKEKLLFYKDDTIALIGGSQSGHGGQNLNRDNLNLYTIGVRKDGSW	Db	181 THVEPPDLDVILVAPKGSGRTVRSLSPREGRGINSPPAVNVTGKAEKAQQLAVAGS
Db	62	GTKENWWERDWPKEKLLFYKDDTIALIGGSQSGHGGQNLNRDNLNLYTIGVRKDGSW	Qy	181 THVEPPDLDVILVAPKGSGRTVRSLSPREGRGINSPPAVNVTGKAEKAQQLAVAGS
Qy	119	KDAVQDGWVPGKNUFPEVDEAISRTGTVIIMLSDAQSETWPALKPQITKGTLTYPFGHGES	Db	245 GYLKTTFEKEYSDLYGERGCLMGGTHGMFLAQYEVTLRERGHSPEAFNETVEATSSL
Db	122	KQAEDEGWGWTGKTFPVEEIKRGSITIMLSDAQETWPALKPQITKGTLTYPFGHGES	Qy	241 GYVYQTTFERVNSDLYGERGCLMGGTHGMFLAQYDVIREGHSPEAFNETVEATSSL
Qy	179	PVEKLTQVKEPTDVVILCAPKGSGRTVRSLSPREGRGINSPPAVYQDVTGEAEKAIAL	Db	305 YPLIGANGMDWYEAACSTTARGGAIQNSPRFKDALKPVNOLYDSDVKGSETORSLDYNS
Db	182	VIFKDQTKIHPKQDVDTWVAPKGSGRTVRSLSPREGRGINSPPAVYQDVTGKAEKAIGL	Qy	305 YPLIGANGMDWYEAACSTTARGGAIQNSPRFKDALKPVNOLYDSDVKGSETORSLDYNS
Qy	239	GVAIGSGYLKTTFEKEYSDLYGERGCLMGGTHGMFLAQYEVTLRERGHSPEAFNETVE	Db	301 YPLIGKGMDDWYDAACSTTARGGAIQNSPRFKDALKPVNOLYDSDVKGSETORSLDYNS
Db	242	AVAVGSGFPIQTTKKEVSDLVGRGCLNGGSPFLAQYDVKRGPAAENETVE	Qy	365 QPDYREKYEAEEMEEIRNLIEWRAGKAVSLRPENQ
Qy	299	EATOSLYPLIIGANGMDWYEAACSTTARGGAIQNSPRFKDALKPVNOLYDSDVKGSETQR	Db	361 QPDYREKLEKELVLTIRNMEIWRVGKETVRLRDKENK
Db	302	EATOSLYPLIIGKGYLDYMPACSTTARGGAIQNSPRFKDALKPVNOLYDSDVKGSETQR	Qy	395
Qy	359	SLDVNSQDPRYERTEAEEMEEIRNLIEWRAGKAVSLRPENQ	Db	Search completed: March 22, 2006, 15:33:24
Qy	400	400	Job time : 127.94 secs	
Db	362	SLEYNSAPNTRYDKELESEIRNLIEWRAGKAVSLRPENK		
RESULT 15				
RN	Q02340	YEAST		
ID	Q02340	YEAST PRELIMINARY;	PRT; 395 AA.	
AC	Q02340;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE		Acetyl-oxo-acid isomerase		
GN	ILV5G;			
OS		Saccharomyces cerevisiae (Baker's yeast).		
OC		Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
OC		Saccharomycetales; Saccharomycetaceae; Saccharomyces.		
OX	NCBI_TaxID=1932;			
RN	[1]			
RP				
RX	Medline:95119792; PubMed:7874731; DOI=10.1007/BF00309925;			
RA	Xie Q.; Jimenez A.;			
RT	"Cloning and molecular analysis of two different ILV5 genes from a			
RT	brewing strain of Saccharomyces cerevisiae."			
RL	Curr. Genet. 26:98-402(1994).			
DR	ENBL; S77495; AAB33578.1; -; Genomic_DNA.			
DR	HSSP; Q01292; 10MG.			
DR	Ensembl; YLR355C; Saccharomyces cerevisiae.			
GO	GO:0004455; F:ketol-acid reductoisomerase activity; IEA.			
GO	GO:0019082; P:branched chain family amino acid biosynthesis; IEA.			
DR	InterPro; IPR00516; Ach_180mrdctse.			
DR	Pfam; PF01450; ILvcC; 1.			
DR	TIGRFAMS; TIGR00445; ilvcC; 1.			
DR	SEQUENCE	395 AA;	44309 MW;	
SQ	2F8BCD94FD7B2AEF CRC64;			
Query Match	71.1%	Score 1489;	DB 2;	
Best Local Similarity	72.2%	Pred. No. 1-8e-98;	Length 395;	
Matches 285;	Conservative 44;	Mismatches 60;	Indels 6; Gaps 3;	
Qy	10	LRPMAQL--ATPVAVQRSSFVAASMMYRATRKA--VAPTOOQIQRGYKTMDFAGHKEQY	64	
Db	2	LRTOAARLICNSVVTAKRTFALATRAAYSRPARYTVPK--MYATRGLKQINFQGTVETV	60	
Qy	65	WERADWPKEKLLFYKDDTIALIGGSQSGHGGQNLNRDNLNLYTIGVRKDGSW	124	
Db	61	YERADWPKEKLLFYKDDTIALIGGSQSGHGGQNLNRDNLNLYTIGVRKDGSW	120	
Qy	125	GWPGKNLPEVDEAISRTGTVIIMLSDAQSETWPALKPQITKGTLVFSHGSPPVFDL	184	
Db	121	GWPGKNLPEVDEAISRTGTVIIMLSDAQSETWPALKPQITKGTLVFSHGSPPVFDL	180	

RT	Identification of yeast proteins from two dimensional gels. ";	Db	301 YPLIGKGMDDYDACSTTARRGALDWPPIFKNALLKPVFQDLYESTNGTETKRSLEFNS 360
RL	Proc. Acad. Sci. U.S.A. 93:1444-1445 (1996).	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	-1- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP (+) = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	-1- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate + NADP (+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	-1- COFACTOR: Magnesium.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	-1- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate; step 2.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	-1- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine from pyruvate; step 2.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	-1- SUBCELLULAR LOCATION: Mitochondrial.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	-1- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	EMBL: XAA969; CAA28643.1; -; Genomic DNA.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	EMBL: U91902; AAB87753.1; -; Genomic_DNA.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	PIR; A24709; A24709.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	HSRP; Q01292; 1QMG.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	IntAct; P06168; -.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	SWISS-2DPAGE; P06168; YEAST.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	Ensembl; YLR355C; Saccharomyces cerevisiae.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	SGD; S00004347; DR.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	GO; GO:0042645; C-mitochondrial nucleoid; IDA.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	GO; GO:0005739; C-mitochondrion; IDA.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	GO; GO:004455; F:ketol-acid reductoisomerase activity; TAS.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	GO; GO:0009082; P:branched chain family amino acid biosynthesis; TAS.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	GO; GO:000002; P:mitochondrial genome maintenance; IMP.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	InterPro; IPR000506; Ach_1somrdrctse.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	PFam; PF01450; ILVC.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
CC	TIGRFAMS; TIGR00465; ilvC; 1.	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
KW	Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
KW	Complete proteome; Direct protein sequencing; Magnesium;	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
KW	Mitochondrion; NADP; Oxidoreductase; Transit peptide.	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
FT	TRANSIT 1 47 Mitochondrion (Potential).	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
FT	CHAIN 48 395	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
FT	NP_BIND 84 93	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
FT	REGION 363 395	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
FT	ACT SITE 171 171	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
SQ	SEQUENCE 395 AA; 44368 MW; D76419A6D68E85E CRC64;	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Query Match	100.0% Score 2071; DB 1; Length 395;	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Best Local Similarity	100.0% Pred. No. 2.1e-141;	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Matches	395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Qy	1 MURTOAARLICNSRVTAKRTFALATRAAAYSRPAAFVPKMFTTRGKQINFGGTETV 60	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Db	1 MURTOAARLICNSRVTAKRTFALATRAAAYSRPAFVPKMFTTRGKQINFGGTETV 60	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Qy	61 YERADWPKEKLLDYPNDTFAIIGKGSYYVNLLSDAQSETWPAIKPLITKGKTLFYSHGFSVFKD 120	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Db	61 YERADWPKEKLLDYPNDTFAIIGKGSYYVNLLSDAQSETWPAIKPLITKGKTLFYSHGFSVFKD 120	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Qy	121 GWPFGKNLFTVEDAIKRGSSYYVNLLSDAQSETWPAIKPLITKGKTLFYSHGFSVFKD 180	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Db	121 GWPFGKNLFTVEDAIKRGSSYYVNLLSDAQSETWPAIKPLITKGKTLFYSHGFSVFKD 180	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Qy	181 THYEPKPDLDVILVAKGKSLRTVSRFKEGRGINSYAVNDVTKRHEKAQALAVIGS 240	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Db	181 THYEPKPDLDVILVAKGKSLRTVSRFKEGRGINSYAVNDVTKRHEKAQALAVIGS 240	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Qy	241 GIVYQTTEREVSNDLVPKGSRTVSLFKEGRGINSYAVNDVTKRHEKAQALAVIGS 240	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Db	241 GIVYQTTEREVSNDLVPKGSRTVSLFKEGRGINSYAVNDVTKRHEKAQALAVIGS 240	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Qy	301 YPLIGKGMDDYDACSTTARRGALDWPPIFKNALLKPVFQDLYESTNGTETKRSLEFNS 360	Db	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395
Db	301 YPLIGKGMDDYDACSTTARRGALDWPPIFKNALLKPVFQDLYESTNGTETKRSLEFNS 360	Qy	361 QDPYREKLEKELDTIRNMEIWKVKEVTKLRPENO 395

Q02340	YEAST PRELIMINARY;	PRT;	395 AA.
AC			
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Acetylhydroy- <i>acid isomero</i> debase.		
GN	Name=ILV5G;		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Bukaryota; Fungi; Ascomycota; Saccharomycetes;		
OC	Saccharomyces; Saccharomycetaceae; Saccharomyces.		
OX	NCBI_TaxID=4932;		
RN	[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].		
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].		
RC	STRAIN=ATCC 2001 / CBS 138;		
RX	PubMed=15225592; DOI=10.1038/nature02579;		
RA	Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,		
RA	Lafontaine I., de Montigny J., Marcil C., Neveuville C., Talla E.,		
RA	Goffard N., Françeur L., Aigle M., Anthouard V., Babour A., Barbe V.,		
RA	Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,		
RA	Boisranc A., Boyer J., Cattolico L., Confinioleri F., de Daruvar A.,		
RA	Desponts L., Fabre E., Fairhead C., Ferry-Dumazet H., Gröppi A.,		
RA	Hantayre F., Henneguin C., Jauhau N., Joyet P., Kachouri R.,		
RA	Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,		
RA	Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,		
RA	Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,		
RA	Swenien D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,		
RA	Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,		
RA	Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,		
RA	Wincker P., Souciet J.-L.,		
RT	"Genome evolution in yeast.";		
RL	Nature 430:35-44(2004).		
EMBL	CR38048; CAG58015.1; -; Genomic_DNA.		
EMBL	ST7415; ABAB33578.1; -; Genomic_DNA.		
DR	GO:00004455; F:ketol-acid reductoisomerase activity; IEA.		
DR	HSSP; Q01232; 1OMG.		
DR	Ensembl; YLR355C; Saccharomyces cerevisiae.		
DR	GO:0005082; P:branched chain family amino acid biosynthesis; IEA.		
DR	InterPro; IPR005056; Ach_isomordctse.		
DR	PFam; PF01450; I1VC; 1.		
DR	TIGRFAMS; TIGR00465; ilVC; 1.		
SQ	SEQUENCE 395 AA; 44309 MW;	2F8BCD94FD7E2ABP CRC64;	
Query Match	Score 97.7%;	Score 2023;	DB 2; Length 395;
Best Local Similarity	97.0%;	Score 6.2e-138;	Length 395;
Matches	383; Conservative	9; Mismatches	3;
		Indels	0;
		Gaps	0;
Qy	1 MIRTOARLICNSRVITAKRTPALATAAYSRPARFVKEMITTRGLQINFGGTIVETV	60	Query Match
Db	1 MIRTOARLICNSRVITAKRTPALATAAYSRPARFVKEMITTRGLQINFGGTIVETV	60	Best Local Similarity
Qy	61 YERADNPREKLLDYFNDTFAILIGYGSQGYGGLNLRDGLNVIIGVRKGASWKAIED	120	Score 91.9%;
Db	61 YERADNPREKLLNYFDTTFAILIGYGSQGYGGLNLRDGLNVIIGVRKGASWKAIED	120	Score 1903;
Qy	121 GWPVKGNLFTYEDATAIKRGSTYMNLLSDAAQESTWPAKTPLITKGKTLFYSHGFSPVFKDL	180	DB 2;
Db	121 GWPVKGNLFSVEDATAIKRGSTYMNLLSDAAQESTWPAKTPLITKGKTLFYSHGFSPVFKDL	180	Length 399;
Qy	181 THVEPPKDLDVTLVAPKGSGRTVSLPKEGRGINSYAVWNDVTGKAHEKQALAVAGS	240	
Db	181 THVEPPKDLDVTLVAPKGSGRTVSLPKEGRGINSYAVWNDVTGKAHEKQALAVAGS	240	
Qy	241 GIVYQTTPEREYNSDLYGERGCLMGGTHGMFLAQYDVLRENGHSPSEAFNETVEATQL	300	
Db	241 GIVYQTTPEREYNSDLYGERGCLMGGTHGMFLAQYDVLRENGHSPSEAFNETVEATQL	300	
Qy	301 YPLIGKYMDDMYDAGSTTARRGALDWYPIPKNAKLPVFDLYESTKNGTETKRSLEFNS	360	
Db	301 YPLIGKYMDDMYDAGSTTARRGALDWYPIPKNAKLPVFDLYESTKNGTETKRSLEFNS	360	
Qy	361 QPDYREKLEKELDTIRNMEIWKGKEVRLRPNQ	395	
Db	361 QPDYREKLEKELVTIRNMEIWKGKEVRLRPNQ	395	
RESULT 4			
ID	Q6FXK6_CANGA	CANGA PRELIMINARY;	PRT;
AC	Q6FXK6_CANGA	399 AA.	
DT	05-JUL-2004 (TREMBLrel. 27, Created)		
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
DE	Candida glabrata strain CBS138 chromosome B complete sequence.		
GN	OrderedLocusNames=CAGL0B030479;		
OS	Candida glabrata (Yeast) (Torulopsis glabrata).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetes; Candida		
OC	Saccharomyces; Saccharomyces cerevisiae; Candida		
OC	mitosporic; Saccharomyces cerevisiae; Candida		
OC	Kluyveromyces lactis		
DE	1140 of Kluyveromyces lactis strain NRRL Y-1140 chromosome A of strain NRRL Y-		
DE	1140 of Kluyveromyces lactis strain NRRL Y-1140 chromosome A of strain NRRL Y-		
RESULT 5			
ID	Q6CY71_KLUTA	KLUTA PRELIMINARY;	PRT;
AC	Q6CY71_KLUTA	397 AA.	
DT	27-Oct-2004 (TREMBLrel. 28, Created)		
DT	27-Oct-2004 (TREMBLrel. 28, Last sequence update)		
DT	27-Oct-2004 (TREMBLrel. 28, Last annotation update)		
DE	140 of Kluyveromyces lactis strain NRRL Y-1140		

GN	OrderedLocusName=KLL0A026739;	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
OS	Kluveromyces lactis (Yeasts).	DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetes;	DE	ACL19WP.
OC	Saccharomycetales; Saccharomyctaceae; Kluveromyces;	GN	Name=ACL19WP;
OX		NCBI_TaxID=28985;	NCBI_TaxID=33169;
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RP	RNA
STRAIN	2359 / IFO 1267 / NRCB 1-1140 / NM37;	RX	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX	PubMed=15229592; DOI=10.1038/nature02579;	RX	STRAIN=ATCC 10895;
RX	Dujon B., Sherman D., Fischer G., Durrels P., Casaregola S.,	RX	PubMed=15001715; DOI=10.1126/science.1095791;
RX	LaFontaine I., March C., Neuveline C., Talla E.,	RX	Dietrich F.S., Voegeli S., Brachet S., Lerch A., Gates K., Steiner S.,
RX	Goffard N., Frangeul L., Aigle M., Anthouard V., Barbe V.,	RX	Mohr C., Poehlmann R., Iudei P., Choi S., Wing R.A., Flavier A.,
RX	Barnay S., Blanchin S., Beckerich J.-M., Beyne B., Bleykasten C.,	RX	Gaffney T.D., Philippin P.;
RX	Bolíbrome A., Boyer J., Cattolico L., Conifianti F., de Daruvar A.,	RX	"The Ashbya gossypii genome as a tool for mapping the ancient
RX	Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,	RX	Saccharomyces cerevisiae genome.";
RX	Hantreave P., Henequin C., Jaujiaux N., Joyet P., Kachouri R.,	RX	Sciencem 304:304-307(2004).
RX	Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,	RX	EMBL; AB016816; AA51031.1; -; Genomic_DNA.
RX	Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,	RX	AGD; ACL198W; -
RX	Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,	RX	GO:0004455; P:ketol-acid reductoisomerase activity; IEA.
RX	Swennen D., Tekala F., Wesczel-Louvel M., Westhof E., Wirth B.,	RX	GO:00016491; P:oxidoreductase activity; IEA.
RX	Zenioi-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,	RX	GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
RX	Bouchier C., Caubron B., Scarpelli C., Gaillard C., Weissbach J.,	RX	DR
RX	Winckler P., Souciet J.-L.	RX	InterPro; IPR00506; AchI_isomrdcte.
RX	"Genome evolution in yeasts."	RX	DR
RX	Nature 430:35-44 (2004).	RX	DR
DR	EMBL; CR382121; CAH02706.1; -; Genomic_DNA.	DR	Best Local Similarity 81.1%; Score 1680; DB 2; Length 394;
DR	GO; GO:0004455; P:ketol-acid reductoisomerase activity; IEA.	DR	Pred. No. 4.1e-113;
DR	GO; GO:0016491; P:oxidoreductase activity; IEA.	DR	Matches 317; Conservative 32; Mismatches 28; Indels 12; Gaps 2;
DR	GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.	DR	KW
DR	InterPro; IPR00006; AchI_isomrdcte.	DR	SEQUENCE 394 AA; 43675 MW; 15AA4E4FB942ACDA3 CRC64;
DR	PFam; PF01450; I1vC; 1.	DR	Query Match 81.1%; Score 1680; DB 2; Length 394;
DR	TIGRFAMS; TIGR00465; ilvC; 1.	DR	Best Local Similarity 81.5%; Pred. No. 4.1e-113;
DR	Complete proteome.	DR	Matches 317; Conservative 32; Mismatches 28; Indels 12; Gaps 2;
DR	SEQUENCE 397 AA; 44189 MW; 7634BBC037ABA9B CRC64;	DR	Qy 18 AKRTPALATAAY-----SRPARYK-----PMITTRGLKQINFSGCTVETYRAD 65
DR	Qy 5 AGRQNIAGTRAAWALSGARARAMPYRSARAPLVSORGVRQISGQTPTVYERAD 64	Db	Qy 66 WPREKULLDPFKNDTFLALIGYGSOCYGGQNLNRDNGLNLVIGVRKDGASMAAIAEDGWPG 125
DR	Qy 65 WPREKULLDPFKNDTFLALIGYGSOCQGGQNLNRDNGLNLVIGVRKDGASMAAIAEDGWPG 124	Db	Db 65 WPREKULLDPFKNDTFLALIGYGSOCQGGQNLNRDNGLNLVIGVRKDGASMAAIAEDGWPG 124
DR	Qy 126 KNLFTVEDAKRGSTVANLISDAQSETPAKELTKLTGKLTGKLYPSHGSFSPVFDLTHVEP 185	Db	Db 126 KNLFTVEDAKRGSTVANLISDAQSETPAKELTKLTGKLTGKLYPSHGSFSPVFDLTHVEP 185
DR	Db 125 ENLPDVRAVERGTVIWMNLISDAQSETPTLRLPTGKLTGKLYPSHGSFSPVFDLTHVEP 184	Db	Db 125 ENLPDVRAVERGTVIWMNLISDAQSETPTLRLPTGKLTGKLYPSHGSFSPVFDLTHVEP 184
DR	Qy 186 PKDLIVILYAPKGSGRTVRSLSFKERGIGNSYAWNDYTGKAHERQALAVAGSGYYQQ 245	Db	Qy 186 PKDLIVILYAPKGSGRTVRSLSFKERGIGNSYAWNDYTGKAHERQALAVAGSGYYQQ 245
DR	Db 185 PKDIVILYAPKGSGRTVRSLSFKERGIGNSYAWNDYTGKAHERQALAVAGSGYYQQ 244	Db	Db 185 PKDIVILYAPKGSGRTVRSLSFKERGIGNSYAWNDYTGKAHERQALAVAGSGYYQQ 244
DR	Qy 246 TTFEREVNSDLYGEGLCMGIGHGMFLAQYDVRLRENGHSPSEAFNETVEATSYPLIG 305	Db	Qy 246 TTFEREVNSDLYGEGLCMGIGHGMFLAQYDVRLRENGHSPSEAFNETVEATSYPLIG 305
DR	Db 245 TTFEREVNSDLYGEGLCMGIGHGMFLAQYDVRLRENGHSPSEAFNETVEATSYPLIG 304	Db	Db 245 TTFEREVNSDLYGEGLCMGIGHGMFLAQYDVRLRENGHSPSEAFNETVEATSYPLIG 304
DR	Qy 306 KYGMMYMDACSTARRGALDWYPTFKNALPKVFDLTVSTNGTETRSLEFNSQPDTR 365	Db	Qy 306 KYGMMYMDACSTARRGALDWYPTFKNALPKVFDLTVSTNGTETRSLEFNSQPDTR 365
DR	Db 305 KHMDDMYMDACSTARRGALDWYPTFKNALPKVFDLTVSTNGTETRSLEFNSQPDTR 364	Db	Db 305 KHMDDMYMDACSTARRGALDWYPTFKNALPKVFDLTVSTNGTETRSLEFNSQPDTR 364
DR	Qy 366 EKLEFELDTIRNMEIWKVGEKVRKLRPEN 394	Db	Qy 366 EKLEFELDTIRNMEIWKVGEKVRKLRPEN 394
DR	Db 365 DRLELQLTRGALDWYPTFKNALPKVFDLTVSTNGTETRSLEFNSQPDTR 393	Db	Db 365 DRLELQLTRGALDWYPTFKNALPKVFDLTVSTNGTETRSLEFNSQPDTR 393
DR	RESULT 7 Q59WWS_CANAL_ID Q59WWS_CANAL PRELIMINARY; PRT; 400 AA.	DR	RESULT 7 Q59WWS_CANAL_ID Q59WWS_CANAL PRELIMINARY; PRT; 400 AA.
DR	AC Q59WWS;	DR	AC Q59WWS;
DR	DT 10-MAY-2005 (TREMBLrel. 30, Created)	DR	DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DR	DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)	DR	DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DR	DE Likely mitochondrial keto isomerase.	DR	DE Likely mitochondrial keto isomerase.
DR	GN Name=ILV5; ORName=Ca019.7733;	DR	GN Name=ILV5; ORName=Ca019.7733;
OS	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.	OS	OS

OC	Saccharomycetales; mitosporic Saccharomycetales; <i>Candida</i> .
OX	NCBI_TaxID=237561;
RN	
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=SC5314;
RX	PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA	Jones T., Federici A., Chibana H., Dungan J., Kajman S., Kajman S., Magee P.T., Magee T.W., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S., Scherer S., "The Diploid Genome Sequence of <i>Candida albicans</i> ," <i>Proc. Natl. Acad. Sci. U.S.A.</i> 101:7329-7334 (2004).
[2]	
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=SC5314;
RX	Pubmed=15123810, DOI=10.1073/pnas.0401648101;
RA	Jones T., Federici A., Chibana H., Dungan J., Kajman S., Kajman S., Magee P.T., Magee T.W., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S., Scherer S., "The Diploid Genome Sequence of <i>Candida albicans</i> ," <i>Proc. Natl. Acad. Sci. U.S.A.</i> 101:7329-7334 (2004).
RT	"The Diploid Genome Sequence of <i>Candida albicans</i> ,"
RL	proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
RN	
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=SC5314;
RX	Pubmed=15123810, DOI=10.1073/pnas.0401648101;
RA	Jones T., Federici A., Chibana H., Dungan J., Kajman S., Kajman S., Magee P.T., Magee T.W., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S., Scherer S., "The Diploid Genome Sequence of <i>Candida albicans</i> ," <i>Proc. Natl. Acad. Sci. U.S.A.</i> 101:7329-7334 (2004).
RT	"Annotation of the Genome of <i>Candida albicans</i> ,"
RL	Submitted (APR-04) to the EMBL/GenBank/DBJ databases.
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/CenBank/DDJB whole genome shotgun (WGS) entry which is preliminary data.
CC	CC EMBL; AAC00100012; EAK94923.1; -; Genomic_DNA.
DR	CC EMBL; AAC00100012; EAK94923.1; -; Genomic_DNA.
KW	Isomerase.
SEQUENCE	400 AA; 44848 MW; ACD3162D05078D81 CRC64;
Qy	3 RTQARL-ICNSRVTAKATLSCRFTSLLANATTRYTAASSAKAMPTPTISRGVKTINFGTB 57
Best Local Similarity	79.1%; pred. No. 3. 6e-12;
Matches	315; Conservative 42; Mismatches 35; Indels 6; Gaps 3;
Db	4 RTTSMEMRATAKATLSCRFTSLLANATTRYTAASSAKAMPTPTISRGVKTINFGTB 63
Qy	58 ETYVERADWPREKLIDYFKNDTFLALIGYSGQGQLNLRDNGNIVTIVSRKGASWKA 117
Db	64 EVVHEPADWPKERLIDYFKNDTFLALIGYSGQGQLNLRDNGNIVTIVSRKGSSWEA 122
Qy	118 IEDGNYPGKKNLFTYDAIKRGSYVNNLSDAAQSTWPALKPLIKGKTLFSGHGSPTF 177
Db	123 VEDGNYPGENLFVDEIAISGTTIINDLSDAAQSTWPALKPLIKGKTLFSGHGSPTF 182
Qy	178 KDLTHVEPKDLDVILVAPKGSGRTVSLPKEGRGINNSYAWNDVTGKAEKAQALAVA 237
Db	183 KDLTHVEPKDLDVILVAPKGSGRTVSLPKEGRGINNSYAWNDVTGKAEKAQALAVA 242
Qy	238 IGSGYVQTFEREVNSDLYGERGCLMGGTHGMFLAQYDYLRENGHSPEAFNETVEAT 297
Db	243 IGSGYVQTFEREVNSDLYGERGCLMGGTHGMFLAQYDYLRENGHTPEAFNETVEAT 302
Qy	298 QSLYPLIGKGMDDMYDNYDACSSTTARGALMPPKFKNALKPVFDLYESTKNGPTKRSIE 357
Db	303 QSLYPLIGKGMDDMYDNYDACSSTTARGALMPPKFKNALKPVFDLYESTKNGPTKRSIE 362
Qy	358 FNSQPDYREKLEKELDTIIRANEIWKVKEVRLRPNQ 395
Db	363 FNSRSIDYKERLLEELQTRNMEIWKVKEVRLRPNQ 400
RESULT	8
Q6BUZ4	DEBHA PRELIMINARY;
ID	Q6BUZ4 DEBHA PRELIMINARY;
AC	Q6BUZ4;
DT	25-Oct-2004 (TrEMBLrel. 28, Created)
DT	25-Oct-2004 (TrEMBLrel. 28, Last sequence update)
DE	Similar to ca CA1933 Cali55 <i>Candida albicans</i> Cal55
DB	reducto-isomerase.
GN	OrderedLocusName=DEHA0104819;
OS	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC	Saccharomycetales; Saccharomycetaceae; Debaromyomycetes.
OX	NCBI_TaxID=4959;

RN	[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP	STRAIN=ATCC 36239 / CBS 767;
RC	Pubmed=15229532; DOI=10.1038/nature02579;
RX	RX Pubmed=15229532; Sherman D., Fischer G., Durress P., Casaregola S., Latontaine I., de Montigny J., Marck C., Neuveglise C., Tally E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babie V., Boirrame A., Boyer J., Cattolico L., Confiolieri F., de Daruvar A., Desponts L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hamiray F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropulos O., Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A., Swanen D., Tekala F., Wesołowski-Louvel M., Westhof B., Wirth B., Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Winkler P., Souciet J.-L.;
RT	"Genome evolution in yeasts.";
RL	Nature 430:35-44 (2004)
DR	EMBL; CR382138; CAG89118.1; -; Genomic_DNA.
DR	GO; GO:0016853; Fisomerase activity; IEA.
DR	GO; GO:004455; F-ketol-acid reductoisomerase activity; IEA.
DR	GO; GO:009082; P-branched chain family amino acid biosynthesis; IEA.
DR	InterPro; IPR005056; AChI _isomrctse.
DR	Pfam; PF01450; ILVc; 1.
DR	TIGRFAMS; TIGR00455; ILVc; 1.
DR	KW Complete proteome; Isomerase.
SQ	SEQUENCE 399 AA; 53D67F203BD09113 CRC64;
Query Match	80.5%; Score 1667; DB 2; Length 400;
Best Local Similarity	80.4%; Score 1665; DB 2; Length 399;
Matches	317; Conservative 39; MisMatches 41; Indels 8; Gaps 1;
Qy	1 MLRTOAARLICNSRVTAKRTPLALATRAAAYSRPAAPEFKPMITTRGLKQINPFGGTVEVY 60
Db	13 MASNNAAKQVASKRALSALANAAARPVARKSIAAPA-----ARGYTKINFQGMDEIV 64
Db	61 YERADWPKRLIDYFKNDTFLALIGYSGQGQLNLRDNGNIVTIVSRKGASWKAATED 120
Db	65 HERADWPKRLIDYFKNDTFLALIGYSGQGQLNLRDNGNIVTIVSRKGASWKAATED 124
Qy	121 GWFYQKNUFLTDEAIKRGSYVNNLSDAQSETWPALKPLTKGKTLFSGHGSPTFKDL 180
Db	125 GWFYGENLEFDVNEAIGKGTYIMNLSDAQSETWESIKPLQITGKTLFSGHGSPTFKEL 184
Qy	181 THYEPKPKDLDVILVAPKGSGRTVSLFKEGRGINNSYAWNDVTGKAEKAQALAVAIGS 240
Db	185 THYEPPTNIDVILVAPKGSGRTVSLFKEGRGINNSYAWNDVTGKAEKAQALAVAIGS 244
Qy	241 GIVYQTTFREVNDSLIGERGCLMGGTHGMFLAQYDYLRENGHSPEAFNETVEATSSL 300
Db	245 GIVYQTTFREVNDSLIGERGCLMGGTHGMFLAQYEVLENQHTSEAFNETVEATSSL 304
Qy	301 YPLIGKGMDDMYDNYDACSSTTARGALMPPKFKNALKPVFDLYESTKNGPTKRSIEBNS 360
Db	305 YPLIGKGMDDMYDNYDACSSTTARGALMPPKFDLYESTKNGPTKRSIEBNS 364
Qy	361 QPDYREKLEKELDTIIRANEIWKVKEVRLRPNQ 395
Db	365 QSDYRLEEELETRISMEIWKVKEVRLRPNQ 399
RESULT	9
Q59XR8	CANAL PRELIMINARY;
ID	Q59XR8_CANAL PRELIMINARY;
AC	Q59XR8;
DT	10-MAY-2005 (TrEMBLrel. 30, Created)
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE	Likely mitochondrial ketol-acid reductoisomerase.
GN	Name=ILV5; ORPNames=Cao19.88;
OS	Candida albicans SC5314.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

NCB_TaxID=237561;

[1] NUCLEOTIDE SEQUENCE.

STRAIN=SC5314;

RX PubMed=15123810; DOI=10.1073/pnas.0401648101;

RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,

RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,

RA Davis R.W., Scherer S.,

RA "The diploid genome sequence of *Candida albicans*,"

RL *Proc. Natl. Acad. Sci. U.S.A.* 101:7329-7334 (2004).

[2] NUCLEOTIDE SEQUENCE.

STRAIN=SC5314;

RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,

RA Roberts J., Person K., Donnelly S., Favoretto S., Tzun K.-W.,

RA Jones T., Scherer S., Agabian N.,

RA "Annotation of the Genome of *Candida albicans*,"

RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

-1- CAUTION: The sequence shown here is derived from an

CC preliminary data.

CC EMBL: AACQ01000106; EAK95225.1; -; Genomic DNA.

KW Isomerase. 400 AA; 44882 MW; FC79162D05078D8C CRC64;

SEQUENCE 400 AA; 44882 MW; FC79162D05078D8C CRC64;

Query Match Score 1663; DB 2; Length 400;

Best Local Similarity 78.9%; Pred. No. 7.1e-112;

Matches 34; Conservative 42; Mismatches 36; Indels 6; Gaps 3;

Sequence 398 AA; 44160 MW; C98C8B7C8AFE26F1 CRC64;

Query Match Score 1663; DB 2; Length 398;

Best Local Similarity 77.6%; Pred. No. 5.1e-106;

Matches 304; Conservative 34; Mismatches 46; Indels 8; Gaps 4;

Query 5 QAR-LIGNSRVITAKRTFALATRAAYSRPAAFRYKPMITRGLKQINFGGTV-62

Db 4 RTTSMRMLATAKATLTSRTTSFLANATTRYTAASSAAKMPITSTRGVKTNFGTE 63

Query 58 ETYVERADPPREKCLDYFKNDTFALIGYSGQYQGQNLNLDGNGLNVIGVRKDGAWSKA 117

Db 64 EVVHERADPKERLDDYFKNDTFALIGYSGQYQGQNLNLDGNGLNVIGVRKDGAWSKA 122

Query 118 IEDGVWPGKLNLFYDAIKRGSYMNLLSDAAQSETWPAAKPLLTGKTYLFGHGFSPVF 177

Db 123 VEDGVWPGKLNLFYDEASRGTIMLSDAAQSETWPAAKPLTGKTYLFGHGFSPVF 182

Query 178 KDLTHVPEPKDLYDVLVIAPKGSERTVRSLPKFKEGRGINSYAVINDYTKGAKHEKAQALAVA 237

Db 183 KDLTHVPEPSNIDVLAIAPKGSERTVRSLPKFKEGRGINSYAVINDYTKGAKHEKAQALAVA 242

Query 238 IGSYYVYQTTFERVNSDLYGRCCLMGHGMFLAQYDVLRENGHSPSEAFNETVEATA 297

Db 243 IGSYYVYQTTFERVNSDLYGRCCLMGHGMFLAQYDVLRENGHSPSEAFNETVEATA 302

Query 298 QSLYPLIGKGYMDYMDAQSSTARRGALDWYPIFKNALPKVFDLYSTKNGTETKRSLE 357

Db 303 QSLYPLIGKGYMDYMDAQSSTARRGALDWYPIFKNALPKVFDLYSTKNGTETKRSLE 362

Query 358 FNSQDQDYRKLKELEDTIRNMEIWKGKEVRKLRPENQ 395

Db 363 FNSRSDYKRLKELEDTIRNMEIWKGKEVRKLRPENQ 400

RESULT 10
Q6CAF8_YARLI
ID Q6CAF8_YARLI PRELIMINARY;
AC Q6CAF8;
DT 25-OCT-2004 (TREMBrel. 28, Created)
DT 25-OCT-2004 (TREMBrel. 28, Last sequence update)

DT Yarrowia lipolytica chromosome D of strain CLIB99 of Yarrowia

DE lipolytica.

GN OrdredokuNames=YAL03135g;

OS Yarrowia lipolytica (Candida lipolytica).

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes;

OC saccharomycetales; Diphodascaceae; Yarrowia.

OX NCBI_TaxID=4952;

RN [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=CLIB 12 / E 150;

RX PMID=15229592; DOI=10.1038/nature02579;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neveglise C., Talla E.,

RA Goffard L., Frangeul L., Aigle M., Antounard V., Babour A.,

RA Barnay S., Blanchin S., Beckerich J.-M., Beyne B., Bleylevasten C.,

RA Boisrame A., Boyer J., Cattolico L., Concanolieri P., de Daruvar A.,

RA Desponts L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,

RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

RA Kerrest A., Koszul R., Lemire M., Lescure I., Ma L., Muller H.,

RA Niclau J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,

RA Swennen D., Tekaya F., Wesolowski-Jouvel M., Westhof E., Wirth B.,

RA Zeniou-Meyer M., Zivanovic Y., Bolotin M., Thierry A.,

RA Bouchier C., Caubron B., Scarpelli C., Gaillardin C., Weissbach J.,

RA Wincier P., Souciet J.-L.;

RL Nature 430:35-44 (2004).

DR EMBL: CR382130 CAG80542.1; -; Genomic DNA.

DR GO; GO:0009082; F:ketol-acid reductoisomerase activity; IEA.

DR InterPro; IPR000506; AchI_isomdrctse.

DR Pfam: PF01150; IIVC; 1.

DR TIGRFAMS; TIGR0465; IIVC; 1.

DR TIGRFAMS; TIGR0465; IIVC; 1.

KW Complete proteome.

SQ Sequence 398 AA; 44160 MW; C98C8B7C8AFE26F1 CRC64;

Query Match Score 1582; DB 2; Length 398;

Best Local Similarity 77.6%; Pred. No. 5.1e-106;

Matches 304; Conservative 34; Mismatches 46; Indels 8; Gaps 4;

Query 5 QAR-LIGNSRVITAKRTFALATRAAYSRPAAFRYKPMITRGLKQINFGGTV-62

Db 12 QARARAVARVATVSARSISMA---TRAPFLKLSAPAV-ARTKTIISNGKEBDIVHE 65

Query 63 RADWPREKLLDFKNDTFALIGYSGQYGOGLNLRDGLNLVIGVRKDGAWSKA 122

Db 66 RADWPQEXLDDYFKNDTFALIGYSGQYGOGLNLRDGLNLVIGVRKDGAWSKA 125

Query 123 VPKGNLFTVDAIKRGSYMNLLSDAQSETWPAAKPLLTGKTYLFGHGFSPVFQDLT 182

Db 126 VPCKNLFDVNEAQKGTINMILSDAQSETWPQIKPLITGKTYLFGHGFSPVFQDLT 185

Query 183 VEPFPKQDQDVLVIAPKGSQRTSFLREGRGNNSYAWNDVTKAVALIAVSGY 242

Db 186 VETPADDVFLVIAPKGSQRTSFLREGRGNNSYAWNDVTKAVALIAVSGY 245

Query 243 VYOTTFEREVNSDLYGRCGLMGHGMFLAQYDVLRENGHSPSEAFNETVEATA 302

Db 246 VYOTTFEREVSDLYGRCGLMGHGMFLAQYDVLRENGHSPSEAFNETVEATA 305

Query 303 LIGKYGMDDYMDACSTTARRGALDWYPIFKNALPKVFDLYSTKNGTETKRSLENSQ 362

Db 306 LIGKYGMDDYMDACSTTARRGALDWYPIFKNALPKVFDLYSTKNGTETKRSLENSQ 365

Query 363 DYREKLEKELDTIRNEIWKYKEVRKLRPEN 394

Db 366 DYRAKFEAELDIRDLEIWRVKEVRKLRPEN 397

RESULT 11
ILV5_NEUCR STANDARD; PRT; 402 AA.

ID ILV5_NEUCR

AC P38674; Q7RVD5; Q8X019.

DT 01-FEB-1995 (Rel. 31, Created)

DT 10-Oct-2003 (Rel. 42, Last sequence update)

DT 13-Sep-2005 (Rel. 48, Last annotation update)

DE Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)

DE (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacti-

reductoisomerase).				
GN Name=ilv-2; ORFNames=B11H24.150, NCU03608;				
OS Neurospora crassa; Fungi; Ascomycota; Sordariomycetes;				
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.				
NCBI TaxID=5141;				
RN [1]				
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RX MEDLINE=91013010; PubMed=1398116; DOI=10.1016/0378-1119(92)90018-K;				
RA Sista H., Borman B.;				
RT "Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-beta-hydroxyacyl reductoisomerase.";				
RL Gene 120:115-118(1992).				
RN [2]				
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RX STRAIN=74-OR23-1A / FGSC 987; MEDLINE=25542210; PubMed=12655011; DOI=10.1093/nar/gkg293;				
RA Manhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,				
RA Hoheisel J.D., Partmann B., Nyakatura G., Kempken F., Maier J.,				
RA Schulte U.,				
RT "What's in the genome of a filamentous fungus? Analysis of the Neurospora genome sequence.";				
RL Nucleic Acids Res. 31:1944-1954 (2003).				
RN [3]				
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RX STRAIN=74-OR23-1A / FGSC 987; MEDLINE=12712197; DOI=10.1038/nature01554;				
RA Galagan J.B., Calvo S.E., Borkovich K.A., Seiler B.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Lehman B., Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Janakiev P., Bell-Pedersen D., Nelson M.A., Werner P.-W., Washburn M., Seitlentrunkoff C.P., Kinsey J.A., Zeiler A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Straben C., Marcotte E., Greenberg D., Roy A., Foley K., Nayor J., Stange-Thomann N., Barrett R., Gneire S., Kamal M., Kamrysselis M., Rauselius E., Bielek C., Rudd S., Frishman D., Kryztofova S., Macino G., Metzger R.L., Perkins D.D., Kroken S., Cogoni C., DeSouza C.P.C., Glass N.L., Orbach M.J., Li W., Pratt R.J., Osmani S.A., Yarden O., Plamann M., Seiler S., Dunlap J.A., Berglund A., Voselker R., Natvig D.O., Alex L.A., Manhaupt G., Ebbple D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.W., RL "The genome sequence of the filamentous fungus Neurospora crassa.";				
RT Nature 422:859-868 (2003).				
RL "The genome sequence of the filamentous fungus Neurospora crassa.;"				
CC -1 - CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+)				
CC = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.				
CC -1 - CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylbutanoate + NADP(+)				
CC = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.				
CC -1 - COFACTOR: Magnesium.				
CC -1 - PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate; step 2.				
CC -1 - PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine from pyruvate; step 2.				
CC -1 - SUBCELLULAR LOCATION: Mitochondrial.				
CC -1 - SIMILARITY: Belongs to the kecol-acid reductoisomerase family.				
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.				
CC EMBL: M94189; AAB00797.1; -; Genomic DNA.				
CC EMBL; AAB00797; -; Genomic DNA.				
CC EMBL; AAB00797; CDD1284.1; -; Genomic DNA.				
CC PIR: JCA428; JC1428.				
CC HSSP; Q9HVA2; 1INP.				
CC InterPro: IPR000505; Ach_isomrdctse.				
CC Pfam: PF01450; Ilvc; 1.				
CC TIGRFAM; TIGR0045; Ilvc; 1.				
CC Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;				
CC Magnesium; Mitochondrion; NADP; Oxidoreductase; Transit peptide.				
CC TRANSIT 1 26 Mitochondrion (Potential).				
CC This Swiss-Prot entry is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.				
CC DR MEDLINE=91013010; PubMed=1398116; DOI=10.1016/0378-1119(92)90018-K;				
CC DR PT CHAIN 27 402				
CC DR PT NP BIND 90 99				
CC DR PT ACT SITE 177 177				
CC DR FT CONFLICT 358 358				
CC DR FT CONFLICT 392 393				
CC DR SQ SEQUENCE 402 AA: 44663 MN: 46795898D2A174 CRC64				
CC Query Match 73 8%; Score 1528.5; DB 1; Length 402;				
CC Best Local Similarity 74.1%; Pred. No. 3.8e-102;				
CC ~ Matches 297; Conservative 39; Mismatches 50; Indels 15; Gaps 4;				
CC Qy 4 TQARLICNSRVTA-KRTP---ALATRAA---AYSPAPARTVPKMTRGKLGQIQINFG 54				
CC Rl 7 TKALRPLARLATPVQRTFVAAVASVAVAPARQV----RGVTTMDPA 60				
CC Query 55 GTVETVYBRADWPRAKLLDYFKNDTFAILIGYSGCGYGGGGLNLRDGLNTIVGRDGASW 114				
CC Db 61 GHKEEYERADWPRAKLLDYFKNDTFAILIGYSGCGQHGGGLNLRDGLNTIVGRNGKSW 120				
CC Query 115 KAAIEGDWYVGPKNLFVYDAIKRGSYVMMILSDAAQSETWPAIKPLLTGKGTLYFSHGFS 174				
CC Db 121 EDAIQDGWYVGPKNLFVDAISRETIVNLLSDAAQSETWPAIKPLLTGKGTLYFSHGFS 180				
CC Query 175 PVPFDLTHVEPKPKDVLVYAPKGSQRTVSLFKEGRGNSYAVWNDVTGKAHQAL 234				
CC Db 181 PVPFDLTKVEVPTDVLVYAPKGSQRTVSLFKEGRGNSPAPYQDTVGKAKEKAVL 240				
CC Query 235 AVAISGSGYYQTTEREVNSDLYGERGCLMGGTHGMLAQDYDVLRENGHSPEAFNETVB 294				
CC Db 241 GVAVGSGLYETFKEVSDLYGERGCLMGGTHGMLAQYEVRERGHSPEAFNETVB 300				
CC Query 295 EATQSPLYPLIGKYMDDYMACSTTARSGALDWYPIFKVNLKQVPUQDLYESTKNGTETKR 354				
CC Db 301 EATQSPLYPLIGKYMDDYMACSTTARSGALDWYPIFKVNLKQVPUQDLYESTKNGTETKR 360				
CC Query 355 SLETPNSQPYREKULEDTIRNMWIKVGYKEVRKLRPENO 395				
CC Db 361 SLETPNSQPYREKULEDTIRNMWIKVGYKEVRKLRPENO 401				
CC RESULT 12 ORFnames=FG1018.1;				
CC ID Q4HY40_GIBZB PRELIMINARY; PRT; 405 AA.				
CC AC Q4HY40;				
CC DT 13-SEP-2005 (TREMBLrel. 31, Created)				
CC DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)				
CC DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)				
CC DE ILV5_NEUCR Ketol-acid reductoisomerase, mitochondrial (Acetohydroxyacid reductoisomerase) (Alpha-keto-beta-hydroxyacyl reductoisomerase),				
CC DE reductoisomerase,				
CC GN ORFnames=FG1018.1;				
CC OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Gibberella.				
CC OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.				
CC OC NCBI_TaxID=29533; RN [1]				
CC RP NUCLEOTIDE SEQUENCE.				
CC RC STRAIN=PH-1; Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bestien V., Bloom T., Boguslavsky L., Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J., Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K., Diaz J.S., Dodge S., Dooley K., Morris L., Elkins T., Engels R., Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J., Gardynska S., Gneire S., Graham L., Grand-pierre N., Hafez N., Jaffe D., Hagan R., Hall J., Horcon L., Huime W., Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A., Kells C., Landers T., Levine R., Lindblad Toth K., Liu G., Lui A., Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J., Matthews C., Mauceli B., McCarthy M., Melidrim J., Menes L., Mihowa T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S., RA				

RA	Rachupka A., Ramasamy U., Raymond C., Retta R., Riese C., Rogov P.,	RA	Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA	Roman J., Schauera S., Schupbach R., Seaman S., Severy P., Smirnov S.,	RA	Ericksen J., Farina A., Faro S., Fischer H.,
RA	Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,	RA	Fitzgerald M., Foley K., Gage D., Galera J., Gerner G.,
RA	Talamas J., Tesfae S., Theodore J., Topham K., Travers M.,	RA	Girke A., Goette A., Graham J., Grandbois E., Gylatsen K., Hafez N.,
RA	Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,	RA	Hagopian D., Hagos B., Hall J., Hatcher B., Heiler A., Higgins H.,
RA	Wu X., Wyman D., Young G., Zainoun J., Zembeck L., Zimmer A., Zody M.,	RA	Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA	Lander E.,	RA	Jaffe D., Jones C., Kamal M., Kamat A., Kamysyssels M., Karlsson B.,
RA	"Submarin" genome sequence";	RA	Kelius C., Kieu A., Kiser P., Labutti K.,
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.	RA	Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
CC	-1 CAUTION: The sequence shown here is derived from an	RA	Lindblad-toh K., Liu X., Lokytsang T., Lokytsang Y., Lucien O.,
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is	RA	Lui A., Ma L.J., Mabbitt R., Macdonald J., Major J.,
CC	preliminary data.	RA	Manning J., Marcella R., Maru K., Mattews C., Mauceli E.,
DR	EMBL; AACM01000419; ERA67345.1; - ; Genomic_DNA.	RA	McCarthy M., McDonough S., McHugh T., Meldrum J., Menes L.,
RW	Isomerase.	RA	Mesirov J., Mihalev S., Mihova T., Mikkelson T., Mlenga V., Moru K.,
SQ	SEQUENCE 405 AA; 44908 MW; 61C6A999723A33FA CRC64;	RA	Mozes J., Mulrain L., Munson G., Nguyen J., Newes C., Nguyen C.,
Qy	2 LRTQARLJNSRVITAKTFALATRAA---AYSRPRAAF-YKPMITTRGLKQINFQGT 56	RA	Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
Matches	Best Local Similarity 72.8%; Score 1507.5%; DB 2; Length 405;	RA	Norbu N., O'Donnell P., Okaoawo B., O'leary S., Omotosho B.,
Matches	Conservative 74.2%; Pred. No. 1-3e-100;	RA	Parker S., Perrin D., Phunkhang P., Pigani B.,
Db	10 LRGPARQLASAPRY-QQTFTSARAARAVARAVARVYASGPQQT-RGVKTMDFAGH 65	RA	Purcell S., Rachupka T., Ramasamy U., Raneau R., Ray V., Raymond C.,
Qy	57 VETYYERAWPREKYLDFEYKNDIFALIGSQSYOGQNLNRDGLNLYTIVGVRKGASWKA 116	RA	Rettie R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
Db	66 KEDYYERAWPQKEXLEYKNDIFALIGSQSYOGQNLNRDGLNLYTIVGVRKGNSWQD 125	RA	Rutman M., Schupbach R., Seaman C., Settipalapati S., Sharpe T.,
Qy	117 AIEPGWVPKRNLFYEDAIKRGSTYVNLISDAQSETPAIRPQLVKGKLYFSGHGSVP 176	RA	Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
Db	126 AEQDGWVACKNLFYEDAIKRGSTYVNLISDAQSETPAIRPQLVKGKLYFSGHGSVP 185	RA	Stetson K., Stone C., Stone S., Strubbs M., Talama S.J., Tchuinga P.,
Qy	177 FDQLTHVEPPKDLDFVLYVAPKGSGRTVRSLSFKERGINSYAWNDYTGKAHEKAQALAV 236	RA	Tenzing P., Testay S., Theodore J., Thoulutsang Y., Topham K.,
Db	245 FDQLKVEPTDIDVLCAPKGSGRTVRSLSFKERGINSFAYVQDVTGKAHEKAQALVG 245	RA	TLI H., Tsamli T., Tsomo N., Vallee D., Vasilev H.,
Qy	237 AIGGGYVYCTTEBEVNSDLYGERGLMGIGHMLQDYLRENGHSPEAFNETVEEA 296	RA	Venkataaraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
Db	246 FDQLKVEPTDIDVLCAPKGSGRTVRSLSFKERGINSFAYVQDVTGKAHEKAQALVG 305	RA	Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadau S.,
Qy	297 TOSIYPLIGKTYGNDYMDACSTTARGALDWYPLFKRNLKPVQDLYESTKNGTETRS L 356	RA	Zimmer A., Zody M., Lander E.;
Db	306 TOSIYPLIGKTYGNDYMDACSTTARGALDWYPLFKRNLKPVQDLYESTKNGTETRS L 365	RA	STRAIN=70-15;
Qy	306 TOSIYPLIGKTYGNDYMDACSTTARGALDWYPLFKRNLKPVQDLYESTKNGTETRS L 365	RL	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
Db	357 EFNQPDYREKLEKBDTTRNMEIWKYREVKLRPENQ 395	RL	[3]
Qy	366 EYNQPDYREKYEAMKEIRELEIWRAKVSRLRPENQ 404	RN	RPNUCLEOTIDE SEQUENCE.
Qy	RESULT 13	Qy	RPNUCLEOTIDE SEQUENCE.
AC	Q5F28_MAGGR PRELIMINARY;	Qy	2 LRTQARLJNSRVITAKTFALATRAAAYSPRAAFVYK-MLTRGLKQINFGGTVETV 60
DT	DT 13-SEP-2005 (TREMBrel. 31, Created)	Qy	Best Local Similarity 73.2%; Pred. No. 1.4e-100;
DT	DT 13-SEP-2005 (TREMBrel. 31, Last sequence update)	Qy	Matches 289; Conservative 44; Mismatches 56; Indels 6; Gaps 3;
DE	DE Hypothetical protein.	Db	10 LRPMAROL--ATPAYQRRTVAASMRVATRKAA--VAPTCQQIQCVKTMDFAGKEQV 64
GN	GN ORFName=MG01808.4;	Qy	61 YERADWPREKLYDFKNDTFALIGSQSYOGQNLNRDGLNLYTIVGVRKGASWKAED 120
OX	OX Sordariomycetes incertae sedis; Magnaporthe.	Db	65 WERADWPKKEKLYFDDTLALIGYSQGHGGLNLRDGLNLYTIVGVRKGASWKAQD 124
RN	RN NCBI_TaxID=242507;	Qy	121 GIVPGKNLFLFTDAIKRGSYMNLLSDAQSETWPALKPLITKGKLYFSGFSPYFKDL 180
RP	RP NUCLEOTIDE SEQUENCE.	Db	125 GIVPGKNLFLFEDDAISGTVMNLLSDAQSETWPALKPLITKGKLYFSGFSPYFKDL 184
RC	RC STRAIN=70-15;	Qy	181 THVEPPKDLDFVLYVAPKGSGRTVRSLSFKERGINSYAWNDYTGKAHEKAQALVG 240
RA	RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E., Anderson S.,	Db	185 TKVEVPTDIDVLCAPKGSGRTVRSLSFKERGINSFAYVQDVTGKAHEKAQALVG 244
RA	RA Altachra M., Allen N., Baldwin J., Bachanteng P., Baldwin J., Barry A.,	RA	David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA	RA Arachchi H., Armbuster J., Bachtang P., Bloom T., Blye J., Boguslavskiy L.,	RA	
RA	RA Bayul T., Bitshasayn B., Brunache A., Butler J., Calixte N.,	RA	
RA	RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,	RA	
RA	RA Campo S., Camara J., Campo K., Chang J., Cheahatang Y., Citroen M.,	RA	
RA	RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Corone C.,	RA	

Qy	241	GYVQTTFEREVNSDLIGGERCCLMGGIHGMPLAQYDVLRENGHSPEAFTQL 300	Qy	185	PPKOLDVILVAPKGSGRTVRSLEKGRGINSYAVWANDVTKAHEKAQALAVAIGSGYV 244
Db	245	GYLKCTTEKEVYSDLYGERCCLMGGIHGMPLAQYEVLRERGHSPSEAFTQL 304	Db	297	VPKDVTILVAPKGSGRTVRSLEKGRGINSSTAVYQDVTGKAKEKAQALAVAIGSGYV 356
Qy	301	YPLIGKGYMDYMDACSTTARRGALDWPIFKNALKPVPFDLYESTKNGSTETKRSLEFNS 360	Qy	245	QTTPREBEVNSDLIGERGCLMGGIHGMPLAQYDVLRENGHSPEAFTQL 304
Db	305	YPLIGANGDMYEA-CTTARRGALDWSPRKDALKPVPFDYQDVKQDSETQRSLDYNS 364	Db	357	ETTEKEVYSDLYGERGCLMGGIHGMPLAQYEVLRERGHSPSEAFTQL 416
Qy	361	QPDYREPKLEKEDLTIRNMEIWKVGEVKLRPENQ 395	Qy	305	GKYMDDYMDACSTTARRGALDWPIFKNALKPVPFDLYESTKNGSTETKRSLEFNSQDQY 364
Db	365	QPDYREKYEAEETIRNLEIWRAGAVRSLRPENQ 399	Db	417	GANGMDWYAACTARRGALDWSPRKDALKPVPFDYQDVKQDSETQRSLEFNSQDQY 476
RESULT 14					
Q4W7W4	ASPFU		Q4W7W4	ASPFU PRELIMINARY;	PRT; 508 AA.
AC			AC		
DT	13-SEP-2005	(TREMBLrel. 31, Created)	DT	15	Q5BAA4_EMENI PRELIMINARY;
DT	13-SEP-2005	(TREMBLrel. 31, Last annotation update)	ID	Q5BAA4;	PRT; 400 AA.
DE	Ketol-acid reductoisomerase.		AC		
DN	ORFName=afu3g1490;		DT	10-MAY-2005 (TREMBLrel. 30, Created)	
OS	Aspergillus fumigatus Af293.		DT	10-MAY-2005 (TREMBLrel. 30, Last sequence update)	
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;		DT	10-MAY-2005 (TREMBLrel. 30, Last annotation update)	
OC	Eurotiales; Trichocomaceae; Aspergillales; Aspergillaceae;		DE	Hypothetical protein.	
NCBI_TaxID	330879; [1]		GN	ORFName=AN526.2;	
RN			OS	Aspergillus nidulans FGSC A4.	
RP			OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;	
RC			OC	Eurotiales; Trichocomaceae; Aspergillaceae;	
STRAIN	AF293;		RN	NCBI_TaxID=227321;	
RA	Nierman W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley J.,		RP	NUCLEOTIDE SEQUENCE.	
RA	Arroyo J., Berriman M., Abe K., Archer D.B., Bernjeo C., Bennett J.,		RC	STRAIN=FGSC A4;	
RA	Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,		RA	Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,	
RA	Farmar M., Fedorova N., Fedorova N., Feldblum T.V., Fischer R.,		RA	Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,	
RA	Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,		RA	Boukhalter B., Butler J., Calvo S.E., Canarata J., Chang J.,	
RA	Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,		RA	Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,	
RA	Haas H., Harris D., Horuchi H., Huang J., Humphrey S., Jimenez J.,		RA	Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,	
RA	Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulikarni R.,		RA	Ericksen J., Faro S., Fitzgerald M., Gage D., Galagan J.,	
RA	Kumagai T., Lafont A., Latge J.-P., Li W., Lord A., Liu C.-M.,		RA	Gardyne S., Gneire S., Graham L., Grand-Pierre N., Hafez N.,	
RA	Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,		RA	Hagopian D., Hagos B., Hall J., Horcon L., Hulme W., Iliev I.,	
RA	Mouyna M.A., Mulligan S., Murphy L., O'Neill S., Pauslen I.,		RA	Jaffe J., Johnson R., Jones C., Kamat A., Karatas A.,	
RA	Pertuis M., Price C., Pritchard B.R., Quail M.A.,		RA	Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,	
RA	Rabinowitz B., Rawlins N., Rajandream M.-A., Reichard U.,		RA	Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,	
RA	Renold H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,		RA	Matthews C., Mauceli B., McCarthy M., Melidrim J., Menes L.,	
RA	Roanning C.M., Rutter S., Salzberg S.L., Sanchez M.,		RA	Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,	
RA	Sanchez J.-C., Saunders D., Seeger K., Squares R., Squares S.,		RA	Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,	
RA	Takeuchi M., Tekaiwa F., Turner G., Vazquez de Aldana C.R., Welton J.,		RA	Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,	
RA	White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,		RA	Rachupka A., Ramasamy U., Raymond C., Resta R., Rize C., Rogov P.,	
RA	Machida M., Hall N., Barrell B., Denning D.W.,		RA	Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,	
RT	"Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus."		RA	Smith C., Spincer B., Strange-Thomson K., Topham K., Traversi M.,	
RT	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.		RA	Talamas J., Tesfaye S., Theodore J., Wilson B., Wilson B.,	
CC	- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.		RA	Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S.,	
CC	SEQUENCE 508 AA; 56353 MW; 09C99AB04D9D2EC CRC64;		RA	Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,	
KW			RA	Lander E.;	
RT	"Genome Sequence of Aspergillus nidulans"; Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.		RT	"Genome Sequence of Aspergillus nidulans"; Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.	
RL			DR	EMBL; AACD010000043; EAA64631.1.; Genomic DNA.	
DR			DR	GO; GO-0004455; P:ketol-acid reductoisomerase activity; IEA.	
GO			DR	GO-0016491; F:oxidoreductase activity; IEA.	
GO			DR	GO-0009082; P:branched chain family amino acid biosynthesis; IEA.	
DR			DR	InterPro; IPR000506; AchI_isomrdsite.	
DR			DR	Pram; PF01450; IIVC; 1.	
DR			DR	TIGRFANs; TIGR000465; IIVC; 1.	
KW			KW	Hypothetical protein.	
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Best Local Similarity	71.9%	Pred. No. 1-56-99;	Best Local Similarity	71.1%	Pred. No. 2-98;
Matches 281;	Conservative 46;	Mismatches 64;	Matches 278;	Conservative 49;	Mismatches 62;
CC		Indels 3; Gaps 1;	CC	Indels 2; Gaps 2;	
CC			CC		
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Db	120	RALRIL--ARVAAPRTVISNALPPALAAATRAAATAPVRGVKTTIAFADSKEVYERA	Db	177	DWPREKLLDVKNDTPALIGCYSGCYGQNLNRQGLNLTIGVRKGASWKAIEGDWP 236
Qy	65	DWPREKLLDVKNDTPALIGCYSGCYGQNLNRQGLNLTIGVRKGASWKAIEGDWP 124	Qy	125	GKNLFTVEDAIKRGSYWVNLSDAQSETWPAIKPLLTGKTLFVSHGFSPVFKDLYVE 184
Db	177	DWPREKLLDVKNDTPALIGCYSGCYGQNLNRQGLNLTIGVRKGASWKAIEGDWP 296	Db	237	GKNLFDLTEAVQKGTIVWNLSDAQSETWPAIKPLLTGKTLFVSHGFSPVFKDLYVE 64

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Db 11 RVARVAAPSSVSALPRSLAKIAANAP--RVAAPVPPVREGVKTISFADSQETYERA 68
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Db 69 DWPREKLQGYKNDTALGGYSGQHGGQNLIRQGNYVIGRKDGASWKEAIQDGVP 128
Qy 125 GKNLPTVEAIKRGSYVMMILSDAQSETWPAIKPLLTGKTLFISHGSPVFKDLTHVE 184
Db 129 GKNLFEVTAVQKGTIVNNILSDAQSETWPTKPLLTGKTLFISHGSPVFKETKVD 188
Qy 185 PPKOLDVILVAPKGSGRTYRSLFKEGRGINSYAWWNYTGKAHEKAOLAYAIGSGVY 244
Db 189 VPSDDVILVAPKGSGRTYRSLFKEGRGINSYAVQDTGNAREKATAMGVAVGSGLY 248
Qy 245 OTTPEREUNVNSDLYGERGCMLMGCIHGMELAQYDVLRENGHSPSRAENETTEATOSLYPLI 304
Db 249 ETTPEKEVYSDLYGERGCMGGTHGMELAQYEVLRERGHSPSRAENETTEATOSLYPLI 308
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Search completed: March 22, 2006, 15:33:25
 Job time : 124.747 secs

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Total number of hits satisfying chosen parameters:	2166443							
Minimum DB seq length:	0							
Maximum DB seq length:	2000000000							
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries							
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Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES								
Result No.	Score	Query	Match	Length	DB	ID	Description	
1	2069	99.2	402	1	ILV5_NEUCR		P3874 neurospora	
2	1860	89.2	400	2	Q52F28_MAGCR		Q52F28 magnaporthe	
3	1819	87.5	405	2	QAHY0_GIB2B		Q4hy40 gibberella	
4	1639	78.6	508	2	Q4WV4_ASPPU		Q4WV4 aspergillus	
5	1611	77.2	400	2	Q5BAA4_EMN1		Q5baa4 aspergillus	
6	1560	74.5	398	2	Q6CA9_YARLJ		Q6caf8 yarrowia li	
7	1542	73.9	399	2	Q6BL24_DEBRA		Q6b624 debaryomyce	
8	1539	73.8	400	2	Q59W5_CANAL		Q59w5 candida alb	
9	1535	73.6	400	2	Q59XR8_CANAL		Q53xr5 candida alb	
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15	1479	70.9	395	2	Q02340_YEAST		Q02340 saccharomyces	
16	1466	70.3	394	2	Q75CM4_ASIGC		Q75cm4 ashbya gossypii	
17	1434	68.8	401	2	Q55QW8_CRNNE		Q55qw8 cryptococcus	
18	1434	68.8	401	2	Q5KEAO_CRNNE		Q5keao cryptococcus	
19	1417	68.0	401	2	Q96V25_CRNB		Q96v25 cryptococcus	
20	1232	625	341	2	Q4P572_USMMA		Q49572 ustilago maydis	
21	1099	52.7	352	2	Q94125_9PUNG		Q91135 pironyces	
22	1086	52.1	362	2	Q5L9J3_BACFN		Q5l9j3 bacteroides	
23	1084	52.0	347	2	Q64P71_BACFR		Q64p71 bacteroides	
24	1075	51.6	359	2	Q8A612_BACTN		Q88612 bacteroides	
25	1071	51.3	344	2	Q84TR5_ASTYPA		Q84tr5 aster yellow	
26	510	24.5	341	2	Q5KWN2_GEOKA		Q5kw2 geobacillus	
27	507	24.3	341	2	Q8R86_BACST		Q81186 bacillus st	
28	497	23.8	333	1	ILVC_AQUAE		Q6789 aquifex aeo	
29	492	23.6	332	1	ILVC_PYRFU		Q8123 pyrococcus	
30	486	23.3	332	1	ILVC_PYRAB		Q9uz9 pyrococcus	
31	484.5	23.2	331	1	ILVC_LISMF		Q71y36 listeria mo	
	33	483	23.2	342	1	ILVC_BACSU		P3753 bacillus su
	34	480.5	23.0	331	1	ILVC_LISMO		Q8y80 listeria mo
	35	472.5	22.7	326	1	ILVC_METKA		Q8t44 methanopyru
	36	470	22.5	335	1	ILVC_METAC		Q8tj4 methanobacillus li
	37	469	22.5	342	2	Q65G17_BACUD		Q65g17 bacillus li
	38	469.5	22.5	581	1	ILV5_PEA		Q82043 pismum sativum
	39	469	22.5	328	1	ILVC_PYRAS		Q8ze1 pyrobaculum
	40	469	22.5	332	1	ILVC_GLOVI		Q7nba0 gloeobacter
	41	466	22.3	578	2	Q65XK0_ORYSA		Q65xk0 oryza sativus
	42	465	22.3	591	1	ILV5_ARATH		Q7575 arabidopsis
	43	463	22.2	335	1	ILVC_SULSO		Q9uox9 sulfolobus
	44	463	22.2	337	1	ILVC_CLOAB		Q97mvo clostridium
	45	463	22.2	341	2	Q5WEN2_BACSK		Q5wen2 bacillus cl

ALIGNMENTS

RESULT 1
ILV5_NEUCR STANDARD:
ID: ILV5_NEUCR STANDARD;
AC: P38674; QBX019;
DT: 01-FEB-1995 (Rel. 31, Created)
DT: 10-OCT-2003 (Rel. 42, Last sequence update)
DT: 13-SEP-2005 (Rel. 48, Last annotation update)
DE: Ketol-acid reductoisomerase, mitochondrial Precursor (EC 1.1.1.86)
(Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxyacyl acyl reductoisomerase).
Name=ilv-2; ORFNames=B11H24.150, NC03608;
OS: Neurospora crassa.
RA: Sista H.; Bowman B.;
RC: Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariaceae; Sordariales; Sordariales; Sordariales; Sordariales; Neurospora.
RN: [1];
RT: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-beta-hydroxyacyl reductoisomerase.;
RL: NCBITaxon ID: 5141;
RN: [1];
RT: Nucleotide sequence of the ilv-2 gene from Neurospora crassa encoding alpha-keto-beta-hydroxyacyl reductoisomerase.;
RL: Gene 120:115-118(1992).
RN: [2];
RT: Nucleotide sequence [large scale genomic DNA].
RN: [3];
RT: Nucleotide sequence [large scale genomic DNA].

CC	= (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.	DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)
CC	-1- NADP (+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.	DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)
CC	-1- CO-FACTOR: Magnesium.	DE	Hypothetical protein.
CC	-1- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-valine biosynthesis; L-valine from pyruvate; step 2.	DE	ORFNames=CG1808.4;
CC	-1- SUBCELLULAR LOCATION: Mitochondrial.	OC	Magnaporthe grisea 70-15.
CC	-1- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.	OC	Sordariomycetes incertae sedis; Magnaportheae; Magnaporthe.
CC	EMBL: M84189; AAB00797.1; -; Genomic DNA.	ON	NCBI_TaxID=242507;
CC	EMBL; ALG70005; CAD21284.1; -; Genomic DNA.	RN	NUCLEOTIDE SEQUENCE.
CC	EMBL; AAB010002700; EAA32099.1; -; Genomic DNA.	RP	STRAIN=70-15;
CC	PIR; JC1428; JCI428.	RA	Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E., Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S., Arachchi H., Armbruster J., Bachartang P., Baldwin J., Barry A., Bayol T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L., Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N., Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M., Collymore A., Considerine T., Cook A., Cooke P., Corum C., David R., Dawe T., Degray S., Dodge S., Dooley K., Dorje P., Dorrie K., Dorris L., Duffey N., Dupes A., Elkinks T., Engels R., Erickson J., Raina A., Pro S., Ferreira P., Fischer H., Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gneire S., Gniorek A., Goettet A., Graham J., Grandbois B., Gyaltsen K., Hafez N., Hagedorn D., Hagos B., Hall J., Hatcher A., Higgins H., Honan T., Horn A., Houde N., Hughes L., Huime W., Husby E., Iliev I., Jaffe D., Jones C., Kamal M., Kamat A., Kamvysseis M., Karlsson E., Kells C., Kieu A., Kisner P., Kodira C., Kulobokas J., Labutki K., Lama D., Landers T., Leeser J., Levine S., Lewis D., Linblad-toh K., Liu X., Lolyitsang T., Lotvitsang Y., Lucien O., Lui A., Ma L., Mabbitt R., McDonald J., MacLean C., Major J., Manning J., Marabella R., Maru K., Matthews C., Mauceli E., McCarthy M., McDonough S., Mcghee T., Meldrim J., Maneus L., Mesirov J., Mihova T., Mikkelson T., Mingle V., Moru K., Mozes J., Mulrain L., Munson G., Nguyen C., Nguyen M., Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C., Norbu N., O'donnell P., Okaivo O., O'leary S., Omotosho S., Purcell S., Raghupka T., Ramasamy U., Rameau R., Ray V., Raymond C., Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P., Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T., Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C., Spencer B., Stalker J., Strange-thomann M., Stavropoulos S., Stenzing P., Tsafaye S., Theodore J., Thoulutsang Y., Topham K., Tewey S., Tsanila T., Tsomo N., Vallee D., Vassilieff H., Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T., Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S., Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L., Zimmer A., Zody M., Lander E., "The genome sequence of Magnaporthe grisea," [2]
CC	SEQUENCE 402 AA; 44623 MW;	RN	NUCLEOTIDE SEQUENCE.
CC	Query Match 99.2%; Score 2069; DB 1; Length 402; Best Local Similarity 99.3%; Pred. No. 3e-138; Matches 399; Conservative 0; Mismatches 1; Indels 2; Gaps 1;	RC	Zhu H., Blackmon B.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
Db	Qy 1 MAARNCTKALRPLARQLATPAVQRRTFVAASAVRASVAVAVAPARQOVRGVTKMDFA 60	RA	Dean R., Mitchell T., Brown D., Pan H., Thon M.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
Db	1 MAARNCTKALRPLARQLATPAVQRRTFVAASAVRASVAVAVAPARQOVRGVTKMDFA 60	RL	-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
Db	61 GHKEEYVERADWPAEKKLDYFKNDTIALIGGSQGHGQGLNLRDNLNVLYVGVRGKSW 120	RN	EMBL/GenBank/DDBJ
Db	61 GHKEEYVERADWPAEKKLDYFKNDTIALIGGSQGHGQGLNLRDNLNVLYVGVRGKSW 120	RP	NUCLEOTIDE SEQUENCE.
Qy	121 EDAIQDWPGKNLFDYDEAISRGTVIWMILSDAAGSETWHIQLITKTLVFSHGS 180	RC	STRAIN=70-15;
Db	121 EDAIQDWPGKNLFDYDEAISRGTVIWMILSDAAGSETWHIQLITKTLVFSHGS 180	RA	Zhu H., Blackmon B.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
Qy	181 PVEKDITKVEVPTDVTDVLYVPAKSGSRTVSLFREGRINSFAYVQDVTGKAKVAL 240	RA	InterPro; IPR00505; Ach isomhardt;
Db	181 PVEKDITKVEVPTDVTDVLYVPAKSGSRTVSLFREGRINSFAYVQDVTGKAKVAL 240	DR	InterPro; IPR00505; Ach isomhardt.
Qy	241 GYAVGSGSYLYETFEKEYSDLYGERGCLMGIGMFLAQEVLERGHSPSEAFNETVE 300	DR	InterPro; IPR09014; Transketolase.
Db	241 GYAVGSGSYLYETFEKEYSDLYGERGCLMGIGMFLAQEVLERGHSPSEAFNETVE 300	DR	PFam; PF01450; IIVc; TIGRFAMS; TIGR00465; IIVc; Hypothetical protein.
Qy	301 EATQSLIPLIGHGMWDFMFDACSTARRGAIIDWTFPKFDALKPVTNLLYOSVRNGDERKR 360	CC	SEQUENCE 400 AA; 44723 MW; 4C89B9E1495BB6D75 CRC64; ID Q52F28; MAGGR PRELIMINARY; PRT; 400 AA.
Db	301 EATQSLIPLIGHGMWDFMFDACSTARRGAIIDWTFPKFDALKPVTNLLYOSVRNGDERKR 360	CC	SEQUENCE 400 AA; 44723 MW; 4C89B9E1495BB6D75 CRC64; ID Q52F28; MAGGR PRELIMINARY; PRT; 400 AA.
Qy	361 SLEYNNSQDPDYRERYEAELEIRNLIEWRAGRK--RSLRPNOK 400	CC	SEQUENCE 400 AA; 44723 MW; 4C89B9E1495BB6D75 CRC64; ID Q52F28; MAGGR PRELIMINARY; PRT; 400 AA.
Db	361 SLEYNNSQDPDYRERYEAELEIRNLIEWRAGRSPRNPOK 400	CC	SEQUENCE 400 AA; 44723 MW; 4C89B9E1495BB6D75 CRC64; ID Q52F28; MAGGR PRELIMINARY; PRT; 400 AA.
RESULT 2	Q52F28 MAGGR PRELIMINARY;	DR	DR
13-SEP-2005 (TREMBLrel. 31, Created)	13-SEP-2005 (TREMBLrel. 31, Last annotation update)	DR	DR

Takeuchi M., Tekaiwa F., Turner G., Vazquez de Aldana C.R., Weldman J., White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K., Machida M., Hall N., Barrell B., Denning D.W.; "Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus"; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is Preliminary data.

DR: AFHF0100002; EAL92139.1; -; Genomic_DNA.

KW: Isomerae. SEQUENCE 508 AA: 56353 MW: 09C99AH04D9D2EC CRC64;

Query Match Score 78.6%; Score 1639; DB 2; Length 508; Best Local Similarity 78.8%; Pred. No. 1..2e-107; Indels 16; Gaps 6; Matches 320; Conservative 35; Mismatches 35; Gapopen 56

Qy 1 MAARNCTKALPRLAROLATPAVORRTFVAAA---SAVRASVAKVAAAPAROQVREVKT 56

Db 113 MASRGLPRLR-LAR-VAAP---RTVSAALPRPALARAAATRAAATAP---VREVKT 162

Qy 57 MDFAGHKKEVHEADWPARKLIDYKNDTALIIGYGSQGHGQCLNLRDNGLAVIYGVKN 116

Db 163 IAFDSLKETVYEAADWPARKLQYKNDTALIIGYGSQGHGQCLNLRDQGLAVIYGVRD 222

Qy 117 GKSWEDAIQDGWPGKNIKFDVDEAISRTGIVNLLSDAQSETPWPKPQITKGKLYF 176

Db 223 GASWKEAICDGWPGKNIKFDLTVAVOKTGIVNLLSDAQSETPWPKPQITKGKLYF 282

Qy 177 HGFSPPVFKDILTKYEVPTDVILVAPKGSGRITVSLFREGRGINSSFAVYQDVTGKAKEK 236

Db 283 HGFSPPVFKELTKYDVPPDVLVAPKGSGRITVRLFREGRGINSSFAVYQDVTGKAKEK 342

Qy 237 AVALGVAVSGYLYETTPEKEYSDLYSRLGRGUMGGHGMELAQYEYLRERGHSPEAFN 296

Db 343 AIAAGVAVSGYLYETTPEKEYSDLYSRLGRGUMGGHGMELAQYEYLRERGHSPEAFN 402

Qy 297 ETVEEATQSLYPLIGAHMDWMDACSTARRAIDWTPKFDALKPVFNLYDSVKNGD 356

Db 403 ETVEEATQSLYPLIGAHMDWMDAATARRAIDWTPKFDALKPVFNLYDSVRDGT 462

Qy 357 ERKSLETSNQSDYRTERAELDEIRNLIEWRAGK--RSLRPENQK 400

Db 463 ETKSLETSNQSDYRTEREYKEMODIRLIEWRAGKAVSRSLPENQK 508

RESULT 5

Q5BAA4_EMENI

ID Q5BAA4_EMENI PRELIMINARY; PRT; 400 AA.

AC Q5BAA4;

DT 10-MAY-2005 (TREMBrel. 30, Created)

DT 10-MAY-2005 (TREMBrel. 30, Last sequence update)

DE Hypothetical protein.

GN ORFName=AN2526_2;

OS Aspergillus nidulans FGSC A4.

OC Eukaryota; Fungi; Ascomycota; Pezizomycetes; Eurotiomycetes; Eurotiidae; Trichocomaceae; Emericellidae.

OX NCBI_TAXID=227321;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FGSC A4;

RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barua N., Bastien T., Boguslavsky L., Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J., Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K., Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R., Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J., Gardyna S., Gneire S., Graham L., Grand-Pierre N., Hafez N., Hsopian D., Hages B., Hall J., Horton L., Hulme W., Iliev I., Jaffe D., Johnson R., Jones C., Kamal A., Karatas A., Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A., Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,

RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L., Mihova T., Mleaga V., Murphy T., Nguyen C., Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S., Rachupka A., Ramasamy U., Raymond C., Reetz R., Ruse C., Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S., Smith C., Spencer B., Strange-Thomann N., Stojanovic N., Stubbs M., Talamas J., Testayre S., Theodore J., Topham K., Travers M., Vassiliev H., Venkataaraman V.S., Vo A., Wang S., Wilson B., Wu X., Wyman D., Young G., Zimmer A., Zembek L., Zody M., Lander E.; "Genome Sequence of Aspergillus nidulans"; Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

RL EMBL; AACD0100043; DR: AACD0100043; EAA64631..1; -; Genomic_DNA.

DR GO: GO-000455; F:ketol-acid_reductoisomerase activity; IEA.

DR GO: GO-0016491; F:oxidoreductase activity; IEA.

DR InterPro: IPR000506; P:branched chain family amino acid biosynthesis; IEA.

DR InterPro: IPR000506; P:branched chain family amino acid biosynthesis; IEA.

DR Pfam: PF01450; I.IVc; 1..

DR TIGRFAMS; TIGR00465; I.IVc; 1.

KW Hypothetical protein.

SQ SEQUENCE 400 AA; 44354 MW; F76A7F2A5AB65PA1 CRC64;

Query Match Score 77.2%; Score 1611; DB 2; Length 400; Best Local Similarity 78.1%; Pred. No. 8..6e-106; Matches 314; Conservative 36; Mismatches 48; Indels 4; Gaps 3;

Qy 1 MAARNCTKALPRLAROLATPAVORRTFVAAA---SAVRASVAKVAAAPAROQVREVKT 60

Db 1 MASRGLPRLR-VARYAAPSIVSALAPRSLAKIANYAAPRVAAAV-VPVRGVKTRIS 58

Qy 61 GHKEEYEEERADPAEKULLDYFKNDTALIIGYGSQGHGQCLNLRDNGLAVIYGVKN 120

Db 59 DSQETVYERADWPRLPREQLEYKNDTALIIGYGSQGHGQCLNLRDNGLAVIYGVKN 118

Qy 121 EDAIQDWWPGKGNLFYDEAISRTGIVNLLSDAAQSETWPHIKPDTKGKLYFSSHGFS 180

Db 119 KEAIQDWWPGKGNLFYDEAISRTGIVNLLSDAAQSETWPHIKPDTKGKLYFSSHGFS 178

Db 239 GVAVGSGLYETTPEKEYSDLYSRLGRGUMGGHGMELAQYEYLRERGHSSEAFNETVE 300

Qy 181 PVFKDILTKYEVPTDVILVAPKGSRTRVSLFREGRGINSFAVYQDVTGKAKEVAL 240

Db 179 PVFKDILTKYEVPTDVILVAPKGSRTRVTLFREGRGINSIAVEQDVTGKAKEVAL 238

Qy 241 GVAVGSGLYETTPEKEYSDLYSRLGRGUMGGHGMELAQYEYLRERGHSSEAFNETVE 300

Db 301 EATQSLYPLIGAHMDWMDACSTARRAIDWTPKFDALKPVFNLYDSVKNGD 360

Db 299 EATQSLYPLIGAHMDWMDACSTARRAIDWTPKFDALKPVFNLYDSVRDGT 358

Qy 361 SILEYNSOPDYRTEREYELDEIRNLIEWRAGK--RSLRPENQK 400

Db 359 SLDYNSQSDYRTEREYCEMOTRDLTEIWRAKGAVRSLRPENQK 400

RESULT 6

Q6CAF8_YARLI

ID Q6CAF8_YARLI PRELIMINARY; PRT; 398 AA.

AC Q6CAF8;

DT 25-OCT-2004 (TREMBrel. 28, Created)

DT 25-OCT-2004 (TREMBrel. 28, Last sequence update)

DE Yarrowia lipolytica chromosome D of strain CJB99 of Yarrowia

DN OrderdLocusNames=YALI0D03135g

OS Yarrowia lipolytica (Candida lipolytica).

OC Saccharomyces; Fungi; Ascomycota; Saccharomyces;

OC Saccharomyces; Dipodascaceae; Yarrowia.

OX NCBI_TAXID=4952;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=CLIB 122 / E 150;

PubMed:15229592; DOI=10.1038/nature02579;	OX NCBI_TaxID=4959;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,	RN [1]
RA Lafontaine I., de Montigny J., March C., Neuveglise C., Talia E.,	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Goiffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,	STRAIN=ATCC-35239 / CBS 767;
RA Barnay S., Blanchard C., Ferry D., Bleykasten C., Talia E.,	RC DOI=10.1038/nature02579;
RA Boisrame A., Blanchard S., Beckrich J.-M., Beyne E., Casaregola S.,	RX Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Despons L., Fabre E., Cattolico L., Confinioli P., de Daruvar A.,	RA Lafontaine I., de Montigny J., March C., Neuveglise C., Talia E.,
RA Hantreux F., Henneguin C., Jauniaux N., Joyet P., Kachouri R.,	RA Goiffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Kerrest A., Koszul R., Lemaire M., Lescu I., Ma L., Muller H.,	RA Barnay S., Blanchard S., Beckrich J.-M., Beyne E., Bleykasten C.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,	RA Boisrame A., Confinioli P., de Daruvar A.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,	RA Boyer J., Cattolico L., Ferry-Dumazet H., Groppi A.,
RA Swennen D., Tekaya F., Wesolowski-Louvel M., Wirth B.,	RA Despons L., Fabre E., Ferry-Dumazet H., Groppi A.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,	RA Hantreux F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,	RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Wincker P., Souciet J.-L.,	RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RT "Genome evolution in yeasts.";	RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RL Nature 430:35-44 (2004).	RA Swennen D., Tekaya F., Wesolowski-Louvel M., Wirth B.,
DR EMBL; OR382130; CAG80542.1; -; Genomic DNA.	RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
DR GO; GO:0016491; P:reducto-isomerase activity; IEA.	RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
DR GO; GO:0009082; P:oxidoreductase activity; IEA.	RA Wincker P., Souciet J.-L.;
DR InterPro; IPR000506; AchI_isomrdctse.	RT "Genome evolution in yeasts.";
DR PFAM; PF01450; ilvc1.1.	RL Nature 430:35-44 (2004).
DR TIGRFAMs; TIGR0465; ilvc1.1.	DR EMBL; CR382130; CAG80542.1; -; Genomic DNA.
DR Complete proteome; 398 AA; 44160 MW; C98CB7C8AFE26F1 CRC64;	DR GO; GO:0016853; P:isomerase activity; IEA.
DR SQ	DR GO; GO:0004455; P:ketoacid reductoisomerase activity; IEA.
Qy 1 MAARNCTKALRPLAROLATPAVQRRTFVAASAVRASVAYKAVAAAPARQOYRGYKTMDDA 60	DR InterPro; IPR000506; AchI_isomrdctse.
Qy 2 1 MSARLSTA---SQRARAVARVATVARSRSISMAATPAFKLSAPAPARTITISN 56	DR InterPro; IPR000506; AchI_isomrdctse.
Db 1 MSARLSTA---SQRARAVARVATVARSRSISMAATPAFKLSAPAPARTITISN 56	DR PFAM; PF01450; ilvc1.1.
Qy 61 GHKEE-VHERADWPARKLDFKNDTLA1LIGYGSQHGGQGNLNRDGLNIVYGRKNGS 119	DR TIGRFAMs; TIGR0465; ilvc1.1.
Db 57 GKEDETHERADWPARKLDFKNDTLA1LIGYGSQHGGQGNLNRDGLNIVYGRKNGS 116	DR Complete proteome; 398 AA; 44160 MW; C98CB7C8AFE26F1 CRC64;
Qy 120 WEDAIQGWVWPKNLDFDEAISRTGIVMNLSDAQSETWPHIFPQITIGKTLFPHGF 179	DR SQ
Db 117 WKAQEQGWWPKNLDFDNEAIGKGTIMNLSDAQSETWPKIPLITIGKTLFPHGF 176	Qy 120 WEDAIQGWVWPKNLDFDEAISRTGIVMNLSDAQSETWPKIPLITIGKTLFPHGF 179
Qy 180 SPVFKDOLTKVTPVTPDYLVYAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKAYA 239	Db 118 WKAQEQGWWPKNLDFDNEAIGKGTIMNLSDAQSETWPKIPLITIGKTLFPHGF 177
Db 177 SPVFKDOLTKVTPVTPDYLVYAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKAYA 236	Qy 180 SPVFKDOLTKVTPVTPDYLVYAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKAYA 239
Qy 240 LGVAVGSGYLVETTERKEVYSDLYGRGRGCLMGIGMPLAQEVYLERGRHSPEAFNEYV 299	Db 178 SPVFKDOLTKVTPVTPDYLVYAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKAYA 237
Db 237 LAIAVSGYYQTTPEKVRSDLYGRGRGCLMGIGMPLAQEVYLERGRHSPEAFNEYV 296	Qy 240 LGVAVGSGYLVETTERKEVYSDLYGRGRGCLMGIGMPLAQEVYLERGRHSPEAFNEYV 299
Qy 300 EAATQSLPLIGAHGMDWIFACSTARGAIDWPKFDALKPVFNLYDSVNGDERK 359	Db 238 LAIAVSGYYQTTPEKVRSDLYGRGRGCLMGIGMPLAQEVYLERGRHSPEAFNEYV 297
Db 297 EAATQSLPLIGAHGMDWIFACSTARGAIDWPKFDALKPVFNLYDSVNGDERK 356	Qy 300 EAATQSLPLIGAHGMDWIFACSTARGAIDWPKFDALKPVFNLYDSVNGDERK 359
Qy 360 RSLEYNSQPDYRERYEAEDEIRNLIWRAAGK--RSLRPEN 398	Db 298 EAATQSLPLIGAHGMDWIFACSTARGAIDWPKFDALKPVFNLYDSVNGDERK 359
Db 357 RSLEFNPSQDYRERYEAEDEIRNLIWRAAGK--RSLRPEN 397	Qy 360 RSLEYNSQPDYRERYEAEDEIRNLIWRAAGK--RSLRPEN 399
RESULT 7	Db 358 RSLEFNPSQDYRERYEAEDEIRNLIWRAAGK--RSLRPEN 399
Q6BL24 DEBHA PRELIMINARY;	AC Q6BL24;
ID Q6BL24- DEBHA PRELIMINARY;	AC Q6BL24;
AC Q6BL24;	DT 25-Oct-2004 (TREMBLrel. 28, Created)
DT 25-Oct-2004 (TREMBLrel. 28, Last sequence update)	DT 25-Oct-2004 (TREMBLrel. 28, Last annotation update)
DB Similar to ca CA1983 Candida albicans CA1983	DB Similar to ca CA1983 Candida albicans CA1983
DB reducto-isomerase.	DB reducto-isomerase.
GN OrderLocusName=DERA0104839;	GN OrderLocusName=DERA0104839;
OS Eukaryota; Fungi; Ascomycota; Saccharomyces; Saccharomyces;	OS Eukaryota; Fungi; Ascomycota; Saccharomyces; Saccharomyces;
OC Saccharomycetales; Saccharomycetales; Debaryomycetes.	OC Saccharomycetales; Saccharomycetales; Debaryomycetes.
Q6BL24 DEBHA PRELIMINARY;	RESULT 8
ID Q6BL24- DEBHA PRELIMINARY;	Q59W5 CANAL
AC Q6BL24;	ID Q59W5;
DT 25-Oct-2004 (TREMBLrel. 28, Created)	AC Q59W5_P CANAL PRELIMINARY;
DT 25-Oct-2004 (TREMBLrel. 28, Last sequence update)	DT 10-MAY-2005 (TREMBLrel. 30, Created)
DB Similar to ca CA1983 Candida albicans CA1983	DB 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DB reducto-isomerase.	DB 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
GN Name=ILV5; ORFName=Ca09.7733;	DE Likely mitochondrial ketol-acid reductoisomerase.
OS	GN Name=ILV5; ORFName=Ca09.7733;

OS	Candida albicans	SGS314.	OX	RN	NCBI_TaxID=2375561;
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		OC	RN	
OC	Saccharomycetales; mitosporic Saccharomycetales; Candida.		OC	RP	NUCLEOTIDE SEQUENCE.
OX			OX	RC	STRAIN=SC5314;
RN			RN	RX	PubMed=15123810; DOI=10.1073/pnas.0401648101;
RP			RP	RA	Jones T., Federici N.A., Chibana H., Dungan J., Kalman S., Magee P.T.,
RC			RC	RA	Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
STRAIN=SC5314;			RA	RA	Davis R.W., Scherer S.;
RX			RA	RA	"The diploid genome sequence of <i>Candida albicans</i> ."
RA			RT	RT	Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004)."
RA			RL	RL	[2]
RA			RN	RN	NUCLEOTIDE SEQUENCE.
RT			RC	RC	STRAIN=SC5314;
RT			RA	RA	Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RT			RA	RA	Roberts J., Persson K., Donnelly S., Favoreto S., Tsung K.-W.,
RT			RA	RA	Jones T., Scherer S., Agabian N.;
RT			RA	RA	"Annotation of the Genome of <i>Candida albicans</i> ."
RL			RT	RT	Submitted (APR 2004) to the EMBL/GenBank/DBJ databases.
CC			CC	CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC			DR	DR	EMBL: AAC001000106; EAK95225.1; -; Genomic_DNA.
CC			KW	KW	Isoenzyme.
DR			SQ	SQ	SEQUENCE 400 AA; 44882 MW; EC791622D05078D8C CRC64;
KW					Query Match 73.6%; Score 1535.5; DB 2; Length 400;
ISomerase.					Best Local Similarity 72.8%; Pred. No. 1.9e-100;
ISomerase.					Matches 295; Conservative 47; Mismatches 52; Indels 11; Gaps 5;
ISomerase.					Qy 1 MAARNCTKALRQLATPAVQRRTVAAASA---VRAVSAYKAVAAAPARQQRVGT
ISomerase.					Db 1 MSFRTSMRMLRATAKAT-LSKRTFSLLANATRTYAASSAKAMPTPIT-SIRGVKT
ISomerase.					56 57 MDFAFGKKEVHERADWPARKLDFKNDTIALGYSQGHGQGLNLRDNGLNLYVGVKN 116
ISomerase.					Db 57 INFQGTEEVHERADWPARKLDFKNDTIALGYSQGHGQGLNLRDNGLNLYVGVKN 115
ISomerase.					Qy 117 GKSWEADAIQDWPGKLNLFVDEAISRGTTVMMILSDAAQSETWPHIKPQITKGKTLFS
ISomerase.					Db 116 GSSWEALAEEDRVPGENLFVDEAISRGTTIMDLISDAAQSETWPHIKPQITKGKTLFS
ISomerase.					176 177 HGFSPVFKDLTKYEVPTDVILVAPKGSSGRTVSLPRGRGINSFAYVQDTGKAEK
ISomerase.					Db 176 HGFSPVFKDLTHVEPPSNIDVLAAPKGSSGRTVSLPRGRGINSFAYVQDTGKAEK
ISomerase.					177 178 AVALGVAVGSGSYLYETFEKSYVSDLYERGCLMGIGHMFQFLAQEVIRERGHSPSEAFN
ISomerase.					Db 177 HGFSPVFKDLTHVEPPSNIDVLAAPKGSSGRTVSLPRGRGINSFAYVQDTGKAEK
ISomerase.					178 179 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 179 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					237 238 ERKRSLEYNSQDYRERYEAELDEINRNLINRAGK-RSLRPEHQ
ISomerase.					Db 238 ERKRSLEYNSQDYRERYEAELDEINRNLINRAGK-RSLRPEHQ
ISomerase.					239 240 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 240 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					241 242 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 242 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					243 244 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 244 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					245 246 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 246 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					247 248 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 248 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					249 250 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 250 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					251 252 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 252 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					253 254 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 254 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					255 256 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 256 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					257 258 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 258 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					259 260 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 260 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					261 262 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 262 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					263 264 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 264 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					265 266 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 266 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					267 268 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 268 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					269 270 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 270 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					271 272 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 272 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					273 274 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 274 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					275 276 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 276 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					277 278 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 278 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					279 280 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 280 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					281 282 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 282 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					283 284 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 284 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					285 286 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 286 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					287 288 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 288 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					289 290 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 290 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					291 292 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 292 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					293 294 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 294 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					295 296 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 296 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					297 298 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 298 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					299 300 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 300 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					301 302 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 302 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					303 304 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 304 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					305 306 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 306 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					307 308 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 308 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					309 310 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 310 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					311 312 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 312 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					313 314 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 314 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					315 316 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 316 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					317 318 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 318 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					319 320 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 320 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					321 322 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 322 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					323 324 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 324 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					325 326 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 326 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					327 328 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 328 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					329 330 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 330 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					331 332 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 332 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					333 334 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 334 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					335 336 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 336 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					337 338 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 338 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					339 340 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 340 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					341 342 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 342 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					343 344 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 344 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					345 346 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 346 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					347 348 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 348 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					349 350 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 350 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					351 352 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 352 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					353 354 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 354 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					355 356 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 356 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					357 358 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 358 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					359 360 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 360 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					361 362 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 362 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					363 364 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 364 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					365 366 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 366 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					367 368 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 368 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					369 370 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 370 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					371 372 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					Db 372 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.					373 374 ETVEEATOSLYPLIGAHGMDWMPFACSTARRGAIIDWTFKDFDALPKVNNLYDSVKNGD
ISomerase.				</	

RESULT 14						
ILV5_SCBHO	ILV5_SCBHO	STANDARD;	PRT;	404 AA.		
ID	ILV5_SCBHO					
AC	P78927 ; 042616 ;					
DT	30-MAY-2000 (Rel. 39, Created)					
DT	16-OCT-2001 (Rel. 40, Last sequence update)					
DT	13-SEP-2005 (Rel. 48, Last annotation update)					
DE	Probable ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxyl acyl reductoisomerase).					
DE	Name=i1v5 ; ORFnames=SPBC56F2.12 ; Schizosaccharomyces pombe (Fission Yeast).					
OS	Eukaryota; Fungi; Ascomycota; Schizosaccharomyces; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.					
OC						
OX						
RN						
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].					
RC	STRAIN=972;					
RX	LINE=1848401; PubMed=11859360; DOI=10.1038/nature724;					
RA	Wood V, Gwilliam R, Rajandream M.A., Lyne M.H., Lyne R., Stewart A., Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S., Brooks S., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moulie S., Mungall K.L., Pearson D., Quail M.A., Rabbinowitsch E., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,					
RA						

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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:02 ; Search time 114.954 Seconds
(without alignments)

1528.885 Million cell updates/sec

Title: US-10-797-248A-3

Perfect score: 2086

Sequence: 1 MAARNCTKALRPLARQLATP.....IRNLEIWRAGKRSRLRPNQK 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqP1980s:*

2: geneseqP1990s:*

3: geneseqP2000s:*

4: geneseqP2010s:*

5: geneseqP2002s:*

6: geneseqP2003as:*

7: geneseqP2003ds:*

8: geneseqP2004s:*

9: geneseqP2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2086	100.0	400	6	ABR64305		Abref4305 Acetohydroxamic acid
2	1860	89.2	400	6	ABR64306		Abref4306 Acetohydroxamic acid
3	1856	89.2	400	9	ABR16807		Abref16807 M Grisea
4	1856	89.0	402	6	ABR64303		Abref4303 Acetohydroxamic acid
5	1658	79.5	403	9	ADV16810		Advf16810 M Gramini
6	1633	78.3	396	6	ABJ26477		Abf26477 Aspergillus
7	1633	78.3	508	6	ABJ26502		Abf26502 Aspergillus
8	1604	76.9	388	6	ABJ25902		Abf25902 Aspergillus
9	1604	76.9	500	6	ABJ25877		Abf25877 Aspergillus
10	1539.5	73.8	400	6	AAU15089		Aau15089 Protein e
11	1539.5	73.8	400	5	ABP73238		Abp73238 Candida a
12	1508.5	72.3	395	6	ABR64304		Abref4304 Acetohydroxamic acid
13	1508.5	72.3	395	7	ADK64188		Adf64188 Disease t
14	1423.5	68.2	409	7	ADB70124		Adb70124 C. neofor
15	1084.5	52.0	347	6	ABU20976		Abu20976 Protein e
16	486	23.3	332	4	AAB96356		Aab96356 Purative
17	486	23.3	586	2	AAV26182		Aav26182 Soybean a
18	483	23.2	342	4	AAU01250		Aau01250 B. subtilis
19	480.5	23.0	331	5	ABB48168		Abb48168 Listeria
20	480.5	23.0	331	6	ABU32456		Abu32456 Protein e
21	473	22.7	579	2	AAY26183		Aay26183 Wheat ace
22	473	22.7	579	2	AAY26180		Aay26180 Corn acet
23	473	22.7	585	8	ADX93651		Adx93651 Plant ful
24	473	22.7	586	8	ADX88429		Adx88429 Plant ful

ALIGNMENTS

RESULT 1
ABR64305 standard, protein; 400 AA.

ID ABR64305
XX

AC ABR64305;
XX

DT 16-SEP-2003 (first entry)
XX

DE Acetohydroxyacid isomero-reductase.
XX

KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomero-reductase.
XX

OS Neurospora crassa.
XX

XX

PR 2001FR-00011689.
XX

XX 10-SEP-2001; 2001FR-00011689.
XX

PA (AVET) AVENTIS CROPSCIENCE SA.
XX

PA (AVET) AVENTIS CROPSCIENCE SA.
XX

PI Dumas R. Lebrun MH, Zundel JL, Effantin G, Morin V;
XX

DR WPT; 2003-405775/39.

Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid isomero-reductase.

PT PR PT PT

PT PT PT PT

Claim 2; Fig 1; 66pp; French.

The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxy acid isomero-reductase. (I) are used for curative or preventive treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxy acid isomero-reductase, used to illustrate the invention

XX

Sequence 400 AA;

Query Match 100.0%; Score 2086; DB 6; Length 400;

Best Local Similarity 100.0%; Pred. No. 2.1e-191;

Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MAARNCTKZLRLAROLATPAVQRTTFVAAASAVRASYAKAVAAAPAROQVRGKTMDF A 60	Query Match 89.2%; Score 1860; DB 6; Length 400;
Db	1 MAARNCTKZLRLAROLATPAVQRTTFVAAASAVRASYAKAVAAAPAROQVRGKTMDF A 60	Best Local Similarity 87.1%; Pred. No. 1.2e-169; Mismatches 350; Conservative 34; Indels 4; Gaps 2;
Qy	61 GHREEVHEADWPBKLLDFKNDTLALIGYGSQGHGQLNLRDNGLNIVYGVRKNSKW 120	Qy 1 MAARNCTKZLRLAROLATPAVQRTTFVAAASAVRASYAKAVAAAPAROQVRGKTMDF A 60
Db	61 GHREEVHEADWPBKLLDFKNDTLALIGYGSQGHGQLNLRDNGLNIVYGVRKNSKW 120	Db 1 MSARGFSKALMRQLATPAVQRTTFVAASSMVRAT - RKAAPATQQIGVKTMDF A 58
Qy	121 EDA1QDGWVPGKNUFLFDVDAEISRTTIVNLLSDAAOSETWPHIKPQITKGKTLYSFHGS F 180	Qy 61 GHKEEYHERADWPBKLLDFKNDTLALIGYGSQGHGQLNLRDNGLNIVYGVRKNSKW 120
Db	121 EDA1QDGWVPGKNUFLFDVDAEISRTTIVNLLSDAAOSETWPHIKPQITKGKTLYSFHGS F 180	Db 59 GHKEEYHERADWPBKLLDFKNDTLALIGYGSQGHGQLNLRDNGLNIVYGVRKNSKW 118
Qy	181 PVEFDLTKVEVPTDVIDVILVAKPGSGRTVRLSPREGINNSFAYQDVTGKAKEKAV A 240	Qy 121 EDA1QDGWVPGKNUFLFDVDAEISRTTIVNLLSDAAOSETWPHIKPQITKGKTLYSFHGS F 180
Db	181 PVEFDLTKVEVPTDVIDVILVAKPGSGRTVRLSPREGINNSFAYQDVTGKAKEKAV A 240	Db 119 KDAVQDGWVPGKNUFLFDVDAEISRTTIVNLLSDAAOSETWPHIKPQITKGKTLYSFHGS F 178
Qy	241 GVAVGSGVYIYETTPEKEYTSDLYGERGCLMGGTHGMFLAQEVYLRGHSRSPSEAFNETV E 300	Qy 181 PVEFDLTKVEVPTDVIDVILVAKPGSGRTVRLSPREGINNSFAYQDVTGKAKEKAV A 240
Db	241 GVAVGSGVYIYETTPEKEYTSDLYGERGCLMGGTHGMFLAQEVYLRGHSRSPSEAFNETV E 300	Db 179 PVEFDLTKVEVPTDVIDVILVAKPGSGRTVRLSPREGINNSFAYQDVTGKAKEKAV A 238
Qy	301 EATOSLYPLIGAHGMDNNFDCACSTTARRGAIDWTPKFDALKPENNLDSYKNGDERKR 360	Qy 241 GVAVGSGVYIYETTPEKEYTSDLYGERGCLMGGTHGMFLAQEVYLRGHSRSPSEAFNETV E 300
Db	301 EATOSLYPLIGAHGMDNNFDCACSTTARRGAIDWTPKFDALKPENNLDSYKNGDERKR 360	Db 239 GVAVGSGVYIYETTPEKEYTSDLYGERGCLMGGTHGMFLAQEVYLRGHSRSPSEAFNETV E 298
Qy	361 SLEYNSQPYRERYEAEELDEIRNLIEWRAKSLRPNOK 400	Qy 301 EATOSLYPLIGAHGMDNNFDCACSTTARRGAIDWTPKFDALKPENNLDSYKNGDERKR 360
Db	361 SLEYNSQPYRERYEAEELDEIRNLIEWRAKSLRPNOK 400	Db 299 EATOSLYPLIGAHGMDNNFDCACSTTARRGAIDWTPKFDALKPENNLDSYKNGDERKR 358
RESULT 2		
	ABR64306 standard; protein; 400 AA.	
XX	ABR64306 standard; protein; 400 AA.	RESULT 3
AC		ADV16807
XX		ID ADV16807 standard; protein; 400 AA.
DT	16-SEP-2003 (first entry)	XX
XX		AC ADV16807;
DE		XX
DE		DN 24-FEB-2005 (first entry)
DE		DE M grisea ketol-acid reductoisomerase IIv5 seqid 6.
OS		XX
OS		XX
OS		KW substrate inhibition; antibiotic; gene disruption;
OS		XX
OS		KW ketol-acid reductoisomerase; IIv5; enzyme.
OS		XX
OS		Magnaporthe grisea.
OS		XX
OS		XX
OS		PN WO2004104176-A2.
PN		XX
PN		PD 02-DEC-2004.
PD		XX
PD	14-MAR-2003.	XX
XX		PP 17-MAY-2004; 2004WO-US015404.
XX		XX
PP	10-SEP-2001; 2001FR-000011689.	PR 15-MAY-2003; 2003US-0470947P.
XX		PR 19-MAY-2003; 2003US-0471615P.
PR	10-SEP-2001; 2001FR-000011689.	PR 21-MAY-2003; 2003US-0472242P.
XX		XX
PA	(AVET) AVENTIS CROPSCIENCE SA.	(PARA-) PARADIGM GENETICS INC.
XX	Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;	XX
XX	WPI; 2003-405775/39.	XX
DR	N-PSDB; ACCB0185, ACCB0186.	XX
XX	PT Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid isomerase.	XX
PT	PT The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (1) of acetohydroxyacid isomerase.	XX
PT	PT (1) are used for curative or preventive treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxy acid isomerase, used to illustrate the invention.	XX
PS	PS Sequence 400 AA;	XX
CC	CC The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (1) of acetohydroxyacid isomerase.	XX
CC	CC (1) are used for curative or preventive treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxy acid isomerase, used to illustrate the invention.	XX
SQ	SQ Claim 48; SEQ ID NO 6; 179pp; English.	PS

XX 02-DEC-2004 .
 XX 17-MAY-2004; 2004WO-US015404 .
 XX 15-MAY-2003; 2003US-0470947P .
 PR 19-MAY-2003; 2003US-0471615P .
 PR 21-MAY-2003; 2003US-0472242P .
 XX (PARA-) PARADIGM GENETICS INC .
 XX DR 2005-021202/02 .
 XX DR N-ESDB; ADV16802, ADV16808, ADV16809 .
 XX Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoyltransferase (OCtase) or keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound .
 XX PS SEQ ID NO 9; 179pp; English .
 XX The invention describes a method of identifying a test compound as a candidate for an antibiotic comprising contacting ornithine carbamoyltransferase (OCtase) or keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound . The method comprises: contacting OCtase polypeptide, keto-acid reductoisomerase polypeptide, or fungal pathogenicity-confering gene with a test compound ; and detecting the presence or absence of binding between the test compound and the polypeptide or gene, where binding indicates that the test compound is a candidate for an antibiotic . Also described are: an isolated nucleic acid comprising a nucleotide sequence encoding a polypeptide having at least 50% sequence identity to, or having at least 10% of the activity of, 400, 403 or 469 amino acids; and an isolated polypeptide consisting essentially of the amino acid sequence of 400, 403 or 469 amino acids . The methods are useful for identifying inhibitors of ornithine carbamoyltransferase, keto-acid reductoisomerase, and fungal pathogenicity-confering gene as antibiotics . This is the amino acid sequence of *Mycosphaerella graminicola* keto-acid reductoisomerase KAR1 .
 XX SQ Sequence 403 AA;
 Qy 79.5%; Score 1658; DB 9; Length 403;
 Best Local Similarity 78.4%; Pred. No. 3.2e-150;
 Matches 315; Conservative 40; Mismatches 43; Indels 4; Gaps 2;
 Db 1 MAARNCTTALPLRQLATPAVQRTTVAASAVRASY-AVKAAPAAPARQVRGVKTM 58
 1 MASKNATLARSLIRQLKPAQVQQRSEFVAVANASRSPSLVPAQAKVSAFVQVRGAKTV 60
 Qy 59 FASGKEEVYHERADMPAEKFLDVKNDTLALIGYSGQHGGQNLDRQGLNLYTVGRKGK 118
 61 FAGDKEYFVERDDWPREKLEFKNDTLALIGYSGQHGGQNLDRQGLNLYTVGRKGGA 120
 Qy 119 SWDAIQGWPKEPKNLFDYDEAISRGTLVMMNLSDAQSETWPHIPEQITGKTLYFSGH 178
 121 SWKEAEGPQWVEKRNLPIDTAIGKGTLMNNTLSDAQSETWPHIKPLTKGKTLYFSGH 180
 Qy 179 FSPVPKDQLTKEVPTDIDVILAPKGSGCTVSLPRIGGINSFAYQDTGKAKEKAV 238
 181 FSPVVKDQTKVEPTDIDVILAPKGSGRTVTLFKEGRGINSIAIFQDTGKAKEKAV 240
 Qy 239 ALGVAVGGYLZETTFFKEVPSDLYGRGLCMLGGIHMFLAQEYLERGHSPSEAFNET 298
 241 ALGVAVGGYMMKTFKEVPSDLYGRGLCMLGGIHMFLAQEYLERGHSPSEAFNET 300
 Qy 299 VEEATQSLXPLGKNGMDYMEACSTIARRGAIDWTPKFDALKPVENNNYDSVKGDER 358
 Db 301 VEEATQSLXPLGKNGMDYMEACSTIARRGAIDWWSKRKFETLKVPEELYDSVKGKET 360
 Qy 359 KRSLEIYNQPDYRVERVEAELDEIRNLEIWRAGK--FSLRPN 398
 Db 361 QPTMEFAGRKQYEAPEKEMEIRNLEIWRAGKAVFSLRPN 402

RESULT 6
 ABJ26477 ID ABJ26477 standard; protein; 396 AA .
 XX AC ABJ26477;
 XX DT 16-APR-2003 (first entry)
 XX DE Aspergillus fumigatus essential gene protein #1135 .
 XX KW Fungicide; cytostatic; essential gene; *Aspergillus fumigatus*; infection; cancer; contamination; biofilm; antibody; immune response .
 XX OS Aspergillus fumigatus .
 XX PN WO200286090-A2 .
 XX PD 31-OCT-2002 .
 XX PP 23-APR-2002; 2002WO-US011142 .
 XX PR 23-APR-2001; 2001US-0285597P .
 PR 27-APR-2001; 2001US-0287066P .
 PR 05-JUN-2001; 2001US-0295990P .
 PR 09-JUL-2001; 2001US-0303999P .
 PR 31-AUG-001; 2001US-0316362P .
 PA (ELIT-) ELUTRA PHARM INC .
 XX PI Jiang B, Tishkoff D, Zamudio C, Broshkin AM, Hu W, Lemieux SM;
 XX DR WPI; 2003-093124/08 .
 XX PT New purified or isolated nucleic acids of essential genes of *Aspergillus fumigatus*, useful for treating or preventing infections by *A. fumigatus*, or for treating a non-infectious disease in a subject e.g. cancer .
 XX PS Disclosure; Page; 175pp; English .
 XX CC The invention relates to novel purified or isolated nucleic acids of essential genes of *Aspergillus fumigatus*. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as *A. fumigatus*, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by *A. fumigatus*, or to prevent or inhibit formation on a surface of a biofilm comprising *A. fumigatus*. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of *A. fumigatus* to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case of virulence factors. This sequence represents a protein of one of the essential genes of *Aspergillus fumigatus* of the invention .
 XX SQ Sequence 396 AA;

Query Match Score 1633; DB 6; Length 396;
 Best Local Similarity 78.6%; Pred. No. 7.9e-148;
 Matches 319; Conservative 35; Mismatches 36; Indels 16; Gaps 6;

Qy 1 MAARNCTKALRPLAROLATPAVORTTFVAAA---SAVVASVAKAVAAPARQOVRGVET 56
 Db 1 MASRGELPRAK-LAR-VAAP---RIVSIALPRLPALARATRAVAASTAP---VRGVET 50

Qy 57 MDFAGHKEYVERADWPAKELDVKYPTNDTLALIGYSQCHGQGLNLRDINGLNIVGVRN 116
 Db 51 IAFADSKETYERADWPREKLYQEPYKPTNDTLALIGYSQCHGQGLNLRDQSLNIVGVRD 110

Qy 117 GKSWEAIIQDWPVGKNLFDVDEAISRGTVWNLSDAQSGETWPHIKPQTKGKLYFS 176
 Db 111 GASWKEAIQDWPVGKNLFDLTEAQKGTVWNLSDAQSSETWPHIKPQTKGKLYFS 170

Qy 177 HGFSPVFKDILTKVEYPTDWDVILVAPKGSGRTVRSLFREGRGINSFAYVQDVTGKAKER 236
 Db 171 HGFSPVFKELTKVDPKDWDVILVAPKGSGRTVRLFREGRGINSIAYVQDVTGKAKER 230

Qy 237 AVALGVAVGSGSYLYETTTEKEVYVSDLYGEGCLMGGIHGMFLAQEVBLERGHSPSEAFN 296
 Db 231 AIAMGVAVGSGSYLYETTTEKEVYVSDLYGEGCLMGGIHGMFLAQEVBLERGHSPSEAFN 290

Qy 297 ETVEEATQSLYPLIGHGMDFDAGCTSTARRGALDWTPKFDALKPVPFNLYDSVKNQD 356
 Db 291 ETVEEATQSLYPLIGHGMANGDMMYAACTSTARRGADWSSRFKDITKPIFNEILDSVRDT 350

Qy 357 ERKRSLEYNSQDTRYERAEDEIRNLTEIWRAKGR--SLRPENQK 400
 Db 351 ETKRSLEYNSQDTRYKEKEMQDIRLLEIWRAKAVGSLRPENQK 396

RESULT 7
 ABJ26502 standard; protein; 508 AA.
 AC ABJ26502;
 DT 16-APR-2003 (First entry)
 XX Aspergillus fumigatus essential gene protein #1160.
 KW Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response;
 XX Aspergillus fumigatus.
 PN WO200286090-A2.
 XX 31-OCT-2002.
 PD 23-APR-2002; 2002WO-US013142.
 XX WPI: 2003-093124/08.
 PR 23-APR-2001; 2001US-0285697P.
 PR 27-APR-2001; 2001US-0287066P.
 PR 05-JUN-2001; 2001US-0295890P.
 PR 09-JUL-2001; 2001US-0303899P.
 PR 31-AUG-2001; 2001US-0316362P.
 XX (BLIT-) BLITRA PHARM INC.
 PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;
 XX WPI: 2003-093124/08.
 XX DR 2002-09302 standard; protein; 388 AA.
 PT PT ABJ25902;
 PT PT AC 2003 (first entry).
 PT PT DT 16-APR-2003 (first entry).
 XX Aspergillus fumigatus essential gene protein #560.
 DE XX KW Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 CC XX cancer; contamination; biofilm; antibody; immune response.
 CC The invention relates to novel purified or isolated nucleic acids of

CC with which binding occurs or to identify inhibitors of the binding
 CC interaction. The polypeptides may be used to raise antibodies or to
 CC elicit immune response, as a reagent in assays designed to quantitatively
 CC determine levels of the protein in biological fluids, as a marker for
 CC host tissues in which pathogenic organism invade or reside, and to
 CC isolate correlative receptors or ligands in the case or virulence
 CC factors. This sequence represents a protein of one of the essential genes
 CC of *Aspergillus fumigatus* of the invention

SQ Sequence 500 AA;

Query Match 76.9%; Score 1604; DB 6; Length 500;
 Best Local Similarity 78.7%; Pred. No. 6.9e-145; Indels 14; Gaps 5;
 Matches 311; Conservative 35; Mismatches 35; Indels 14; Gaps 5;

Qy 1 MAANCTKALRPLARQLQATPAVQRTTFVAA---SAVASVAVRAVAPARQVQYGT 56

Db 113 MASRLPLAR-LAR-VAAP---RTVIVALPRPALAGATRAVAASTP---VRGTYT 162

Qy 57 MDFAGHKEYVERADWPALKLDDYFKNDTIALIGYSQSGHGOGLNLRDGLNYTGVRN 116

Db 163 IAFADSKEVYERADWPALKLDDYFKNDTIALIGYSQSGHGOGLNLRDGLNYTGVRN 222

Qy 117 GKSNEADQIDGWPQKNLPDYDEAISRGTVIWNLLSDAQSETMPHKEQITGKTLYF 176

Db 223 GASHKBAIQDQWPKSPNKLPLDTEAVQKGTVIWNLLSDAQSETMPHLKLTGKTLYF 282

Qy 177 HGFSPVFKDLTKVETPTDQDVLVAPKGSGERTVSLFRGRRGINSFAYVQDTGKAKK 236

Db 283 HGFSPVFKDLTKVDPKDVILVAPKGSGERTVSLFRGRRGINSFAYVQDTGKAKK 342

Qy 237 AVALGVAVSGCYLYETTFKREKVSPLYGRGCLMGCGIHMFLAQYEYLRERGHSPSEAFN 296

Db 343 ALANGVAVSGCYLYETTFKREKVSPLYGRGCLMGCGIHMFLAQYEYLRERGHSPSEAFN 402

Qy 297 ETVEEATQSYPLIGAHGMDMFDACSTARRGAIDWPKFQDALKPYNLYDSVNGD 356

Db 403 ETVEEATQSYPLIGAHGMDMYYAACSTARRGAIDWPKFQDALKPYNLYDSVNGT 462

Qy 357 ERKSLSEYNSQDPDREYAEELDTRNLLEWRAGK 391

Db 463 ETKRSLEYNSQDPDREYKEKMDIRDLEIWRAGK 497

RESULT 1.0
 ID AAU15089 standard; protein; 400 AA.
 XX AAU15089;
 XX DT 04-DEC-2001 (first entry)
 XX DE Protein encoded by *C. albicans* essential gene *CAYLR355C* (IIV5).
 XX Gene identification; essential gene; GRACE; pathogenic fungus;
 XX gene replacement and conditional expression; fungal infection.
 XX Candida albicans.

QX WO200160975-A2.

PN 23-AUG-2001.

PP 20-FEB-2001; 2001WO-US005551.

PR 18-FEB-2000; 2000US-0163534P.

PA (ELIT-) ELITRA PHARM INC.

PI Roemer T, Jiang B, Boone C, Bussey H;

XX WO200253728-A2.

DR WPI: 2001-489080/53.

N-PSDB; AAS23417.

XX PT Identifying genes essential to fungal metabolism and identifying
 CC potential therapeutic agents that target these genes.
 PT XX
 PS Claim 43; Page 222-223; 324pp; English.

XX The present invention relates to novel methods for constructing fungal
 CC strains useful for identification and validation of gene products as
 CC targets for therapeutic agents, for creating a collection of identified
 CC essential genes, and screening assays for the discovery of new drugs. The
 CC invention provides the GRACE (gene replacement and conditional
 CC expression) method for the construction of mutant organisms referred to any
 CC organism, particularly a pathogenic fungus e.g. *Candida albicans*,
 CC *Aspergillus fumigatus* and *Cryptococcus neoformans*. The methods are useful
 CC to identify agents that may be used in the treatment of fungal
 CC infections. AAU15053-AAU15113 represent proteins encoded by *C. albicans*
 CC essential genes.
 XX SQ Sequence 400 AA;

Query Match 73.8%; Score 1539.5; DB 4; Length 400;
 Best Local Similarity 73.1%; Pred. No. 7.9e-139;
 Matches 296; Conservative 47; Mismatches 51; Indels 11; Gaps 5;
 Qy 1 MAARNCTKALRPLARQLATPAVORYTIVAAAS---VRAVASVAKAVAAAPARQVQYKTT 56
 Db 1 MSFRPTSRMARIATATAK--LSKRTRFLLANATTYTAASSAKAMPIT--SIRGYTT 56
 Qy 57 MDPAGHKEEVHERADWPALKLDDYFKNDTIALIGYSQSGHGOGLNLRDGLNYTGVRN 116
 Db 57 INFGGTEEVHERADWPALKLDDYFKNDTIALIGYSQSGHGOGLNLRDGLNYTGVRN 115
 Qy 117 GRSWEADATQDGWPGKNFDVDAISRETIVWLLSDAQSETWPKPQITGKTLVFS 176
 Db 116 GSSWEAAVEDGWPGENFEVDAISRTTIDMLLSDAQSETWPKPQITGKTLVFS 175
 Qy 177 HGFSPVFKDLTKVETPTDQDVLVAPKGSGRTVSLFREGRGINSFAYVQDTGKAKK 236
 Db 176 HGFSPVFKDLTHVBPSPNIDVLAAPKGSGRTVSLFREGRGINSFAYVQDTGKAKK 235
 Qy 237 AVALGVAVSGCYLYETTFKREKVSPLYGRGCLMGCGIHMFLAQYEYLRERGHSPSEAFN 296
 Db 236 AIAAAIAAGSGYKTYKTPEREVNSDLYGERGCLMGCGIHMFLAQYEYLRERGHSPSEAFN 295
 Qy 297 ETVEEATQSYPLIGAHGMDMFDACSTARRGAIDWPKFQDALKPYNLYDSVNGD 356
 Db 296 ETVEEATQSYPLIGKYMDDYNAACSTARRGAIDWPKFQDALKPYNLYDSVNGD 355
 Qy 357 ERKSLSEYNSQDPDREYAEELDTRNLLEWRAGK - RSLRPNQ 399
 Db 356 ETRKSLFNSRSDYKERLEELQTRNMEIWRVGEVRKLRPENQ 400

RESULT 1.1
 ABP73238 standard; protein; 400 AA.
 ID ABP73238;
 XX AC ABP73238;
 XX DT 30-JAN-2003 (first entry)

XX DE *Candida albicans* essential protein SEQ ID NO 7075.
 XX KW Fungus; Yeast; tetracyclin; Promoter; GRACE strain; biosynthesis;
 XX signal transduction; DNA replication; cell division; growth;
 XX proliferation; *Candida albicans*; fungicide; antifungal.
 XX OS *Candida albicans*.

XX XX PN WO200253728-A2.
 XX XX PD 11-JUL-2002.

XX	26-DEC-2001; 2001WO-US049486.	Db	296 ETYBEATOSLYPLIGKGMDDMYDACSTTARGALLNLEINRAGK- -RSLRPENQ 355
PP	29-DEC-2000; 2000US-0259128P.	Qy	357 ERKSLLEYNQDPPREYEAIRLDEIRNLEINRAGK- -RSLRPENQ 399
PR	20-FEB-2001; 2001US-00792024.	Db	356 ERKSLLEFNRSRDKYKLEELQTIINMEIWRVGRTEVRLRPFENQ 400
PR	22-AUG-2001; 2001US-0314050P.	PA	
XX	(ELIT-) ELITRA PHARM INC.		
XX	Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;	RESULT 12	
PI	WPI; 2002-566694/60.	ID	ABR64304 standard; protein; 395 AA.
XX	DR; ABZ31788.	XX	
XX	XX	AC	ABR64304;
PT	Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.	DT	16-SEP-2003 (first entry)
PT		XX	
XX		DE	Acetohydroxyacid isomerase.
PS	Claim 44; SEQ ID NO 7075; 167pp + Sequence Listing; English.	XX	
XX	The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of <i>C. albicans</i> cell and for treating infection by <i>C. albicans</i> . The present sequence is that of an essential <i>Candida albicans</i> protein used in the method of the invention.	OS	
CC	Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office	PN	
XX	Sequence 400 AA;	PR	2003-405775/39.
CC	Score 1539.5; DB 5; Length 400;	XX	
Best Local Similarity 73.1%; Pred. No. 7.9e-139;	Qy	73.8%; Score 1539.5; DB 5; Length 400;	
Matches 296; Conservative 47; Mismatches 51; Indels 11; Gaps 5;	Db	73.1%; Score 1508.5; DB 6; Length 395;	
Qy	1 MAARNCTKALRPLARLATPAVQRRTFVAAASA---VRASTAVKAVAAPARQQVGVKT 56	Best Local Similarity 73.6%; Pred. No. 7.4e-136;	
Db	1 MSRPTTSNMRALARATAKAT- -LSKRTFLLANATTRTAASSAAKAMTPIT- -SIRGVKT 56	Matches 295; Conservative 39; Mismatches 50; Indels 18; Gaps 5;	
Qy	57 MDFAGHKEBVHERADWPAPKLLDYFNDTLLALIYGSGQHGGGLNLDNGLNIVGEVRK 116	Qy	7 TKALRPLARLATPAVQRRTFVAAASAVRASVAKAVAAPARQQV-----RGVKTMDFA 60
Db	57 IMFGGTEEVHVERADWPAPKLLDYFNDTALIYGSGQHGGGLNLDNGLNIVIGRK- 115	Db	4 TOAARLICNSRVITA- -KRTF- - - - -AYSRPARFVRPMITTRGLKQINFQ 54
Qy	117 HGFSPPVFKDLTKEVPTDVTILVAPKGSRGTYSRSLPREGRINSSPAVYQDVTGKAKEK 236	Qy	61 GHKEEYTHERAQMPAECCLDYFNDTLLALIYGSGQHGGGLNLDNGLNIVGEVRKGSW 120
Db	116 GSSWEAAVBDGWPGENF,FEVDEAISGTTIMDLSDAQSQSTWPHKQPLTEGKTLYFS 175	Db	55 GTVETTYERADWPREKLLDYFNDTALIYGSGQHGGGLNLDNGLNIVGEVRKGSW 114
Qy	177 HGFSPPVFKDLTKEVPTDVTILVAPKGSRGTYSRSLPREGRINSSPAVYQDVTGKAKEK 236	Qy	121 EDAIQDGWPGKNLFLFDDEAISRGTVMLLSDAQSSETWPHIKPLTKGKTLYFPHGFS 180
Db	176 HGFSPPVFKDLTKEVPTDVTILVAPKGSRGTYSRSLPREGRINSSPAVYQDVTGKAKEK 235	Db	115 KAAIEBGWVPSKINLFTVEDA1KRGSTVMNLLSDAQSSETWPHIKPLTKGKTLYFPHGFS 174
Qy	237 AVALGVAVSGSYIYETTFPEKEYSDLYGERGCLMGGHMGMLFLAQYEVTLERGHSPSEAFN 296	Qy	181 PFKDQDTKVEVPTDVTILVAPKGSRGTYSRSLPREGRINSSPAVYQDVTGKAKEKAV 240
Db	236 ATAMAIAGSGYVKTFFREVNSDLYGERGCLMGGHMGMLFLAQYEVTLERGHSPSEAFN 295	Db	175 PFKDQDTKVEVPTDVTILVAPKGSRGTYSRSLPREGRINSSPAVYQDVTGKAKEQAL 234
Qy	297 ETVEEAATOSLYPLIGKGMDDMFACSTTARRGAIDWTPKFDALKPVEVNLYDSTVNGD 356	Qy	241 GVAVGSGYLYETTFPEKEYSDLYGERGCLMGGHMGMLFLAQYEVTLERGHSPSEAFVETVE 300

Db 235 AVAIGSGYVQTTPERBVSNDLYGERGCLMGGIHMFLAQDVLRENGSPSEAFNETTE 294
 Db 301 EATQSYPLIGAHMDWMFDACSTARRGAIIDWTPKFQDALKPWFNNLTDSSVNGDEKR 360
 Qy 295 EATQSYPLIGKGYMDYMDACSTARRGAIIDWTPKFQDALKPWFQDLIESTNGTEIR 354
 Qy 361 SLEYNSQDPRYERYPAELDETRNLBIWRAGK-RSLRPNQ 399
 Db 355 SLEYNSQDPRYERKLERELDITRNMBIWKVGEVRKLRLRPNQ 395

RESULT 13
 ADK64188 ID ADK64188 standard; protein; 395 AA.
 XX AC ADK64188;
 XX DT 06-MAY-2004 (first entry)
 XX DE Disease treating protein complex-derived protein #1281.
 XX KW protein complex; drug target; diagnosis.
 XX OS Unidentified.
 XX PN EP1338608-A2.
 XX PD 27-AUG-2003.
 XX PF 20-DEC-2002; 2002EP-00102902.
 XX PR 20-DEC-2001; 2001EP-00130253.
 XX PA (CELL-) CELLZONE AG.
 XX PI Bauer A, Gavin A, Superti-Purga G, Kuester B, Schultz J, Schulte J;
 PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
 PI Michon A, Lautwein C, Rick J;
 XX WPI: 2003-638460/61.
 DR N-PSDB; ADK64189.
 XX PT New proteins and protein complexes from eukaryotes, useful as targets in drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or disorder in a subject.
 XX Disclosure: SEQ ID NO 2561; 13pp; English.
 XX The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologe or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or prevention of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
 XX SQ Sequence 395 AA;

Db 295; Conservative 39; Mismatches 50; Indels 17; Gaps 5;
 Qy 7 TKAFLPLRQLPLATPAVQRTFVAAAASAVRASVAKAVAAVAPARQV-----REVKTMDFA 60
 Db 4 TQARLICNSRVT-A-KTP-- ALATRAA---ASRPAARPVKPMITRGLQKQINGF 54
 Qy 61 GHKEEVHERADWPAEKLIDYFKNDTALIGYGSQGHGGLNLNDGLNIVGTRNGKSW 120
 Db 55 GIVETVYERADWPKEKLIDYFKNDTALIGYGSQGHGGLNLNDGLNIVGTRNGKSW 114
 Qy 121 EDATQDGWPGPKNLFDVDEAISRGTYIVRNLLSDAAQESTWPHIKPQDTPKGKTYFSGHFS 180
 Db 115 KAALEDGWPGPKNLFVDAIKRGSYVWNLLSDAAQESTWPAKPLLTGKTYFSGHFS 174

Db 181 PVPFDLTVCEVPDQDVILVAPKGSGRTVRSLEPREGQINSPPAYQDVTGKAKEKAVL 240
 Qy 175 PVPFDLTVHEPPKDLTVAPKGSGRTVRSLEPREGQINSPPAYQDVTGKAKEKQAL 234
 Db 241 GYAVGSGTYETTEKEYTSLYGERGCLMGJLHGMPFLAQEVYLTERCHSPSEAFLNETVE 300
 Db 235 AVAISGTYQTFEREVNSDLYGERGCLMGJLHGMPFLAQDVTLRECHSPSEAFLNETVE 294
 Qy 301 EATOSLYPLIGAHMDWMFDACSTARRGAIIDWTPKFQDALKPWFVNGDVERK 360
 Db 295 EATOSLYPLIGKGYMDYMDACSTARRGALDWYPFKRNALKPWFQDLYESTNGTETKR 354
 Qy 361 SLEYNSQDPRYERYAEELDEIRNLIEWKAGK-RSLRPNQ 399
 Db 355 SLEYNSQDPRYERKLERELDITRNMEIWKVGEVRKLRLPENQ 395

RESULT 14
 ADB70124 ID ADB70124 standard; protein; 409 AA.
 XX AC ADB70124;
 XX DT 04-DEC-2003 (first entry)
 XX DE C. neoformans amino acid sequence SEQ ID NO:3168.
 XX KW fungicide; gene therapy; infection.
 XX OS Cryptococcus neoformans.
 XX PN WO2003052076-A2.
 XX PD 26-JUN-2003.
 XX PF 17-DBC-2002; 2002WO-US040225.
 XX PR 17-DBC-2001; 2001US-0341261P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Zamudio C, Broshkin AM;
 XX DR WPI; 2003-533017/50.
 DR N-PSDB; ADBE9041.
 XX PT New nucleic acid, useful for preparing a composition for treating an infection caused by Cryptococcus neoformans.
 XX Claim 9; SEQ ID NO 3168; 136pp; English.
 XX The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence encoding a polypeptide comprising a sequence not given in the specification. A polynucleotide of the invention has fungicide activity, and may have a use in gene therapy. The nucleic acid is useful for preparing a composition for treating an infection caused by Cryptococcus neoformans.
 CC The present sequence represents a C. neoformans sequence of the invention. Note: The sequence data for this patent is not represented in the present sequence repre

Query Match 72.3%; Score 1508.5; DB 7; Length 395;
 Best Local Similarity 73.6%; Pred. No. 7.4e-136;

CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp://wipo.int/pub/published_pat_sequences.
 XX

SQ Sequence 409 AA;

Query Match 68.2%; Score 1423.5; DB 7; Length 409;
 Best Local Similarity 70.2%; Pred. No. 1.2e-127; Mismatches 62; Indels 9; Gaps 3;
 Matches 278; Conservative 47; Gaps 3;

Qy 3 ARNTKALPQLRQALATPVAQORTP-VAAASAVRASVAKVAAPARQVQRGKTMDFAG 61
 Db 4 SRASSNALQALISTASRQYARSSYSSGAAPRAAMTRLGP-----TRGKTKDFAG 57
 Qy 62 HKEEYERADWPALKLDPKNDTLLALIGYGSQGHGQSLNLRDNGLAVIYGRKNGKSW 121
 Db 58 TKEVYERADWPDLQPKNDTLLAMIGYGSQGHGQSLNARDNGLKVYGRKNGKSW 117
 Qy 122 DATODGMYEGKNGKLNFLDVEAISRGTVINMILSDAAQSETWPHIKPQITKGKTLYFSHGFS 181
 Db 118 QAOEDGWGETDPIPEAKNGKTMNMLSDAAQSOQWNEATPLTKGKTYFAGFSV 177
 Qy 182 VFKDLTKVVEPTDYLVAPKGSGRITVSLFREGRGINNSFAYQDVTGKAKEKAVALG 241
 Db 178 VYCEDTHYTPPKDQDYLVAPKGSGRITVTLFREGRGINNSFAYQDVTGKAKEKAVALG 237
 Qy 242 VAVGSGYLWETTPEKEVYSDLYGERCIMGGIHGMFLAQYEVLREGRHSPSSEAFNETVE 301
 Db 238 IAVGSGYLWETTPEKEVYSDLYGERCIMGGIHGMFLAQYEVLREGRHSPSSEAFNETVE 297
 Qy 302 ATOSLYPLJGAHGDWWMPDACPSTTARRGAIDWTPKFKDALKPQVFNLYDSVKGNGDERS 361
 Db 298 ATOSLFLPLIGKMDYMANCSTTARRGAIDWTPKFKDALKPQVFNLYDSVKGNGDERS 357
 Qy 362 LEYNQSDPYRERYAEELDEIRNLFWRAGK--RSLR 395
 Db 358 LEFNRSRKYREDIQLKEEDIDNBWIRAGKTYGLR 393

RESULT 15
 ABU20976 standard protein; 347 AA.
 XX

AC ABU20976;
 XX 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #6503.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Bacteroides fragilis.
 FN WO200271183-A2.
 XX 03-OCT-2002.
 XX 21-MAR-2002; 2002WO-US009107.
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948933.
 PR 25-OCT-2001; 2001US-0342922P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 05-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GD, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 DR N-PSDB; ACA24846.
 XX New antisense nucleic acids, useful for identifying proteins or screening

PT For homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX

SQ Claim 25; SEQ ID NO 48900; 1766p; English.

XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 347 AA;

Query Match 52.0%; Score 1084.5; DB 6; Length 347;
 Best Local Similarity 59.9%; Pred. No. 3.8e-35;
 Matches 206; Conservative 51; Mismatches 84; Indels 8 3; Gaps 2;
 Qy 57 MDPAGHKEEYERADWPALKLDPKNDTLLALIGYGSQGHGQSLNLRDNGLAVIYGRKRN 116
 Db 4 LNFGGVTVENVTREEPFLEKAREVLLKNETIAVIGYGVQPGSOSLNLRDNGFNVICQRP- 62
 Qy 117 GKSWEADAIODGWPVPGNLFDFDEAISRGTVINMILSDAAQSETWPHIKPQITKGKTLYFS 176
 Db 63 GRYYEKAVADGIVPGVGETLFGEBACKGTINCLLSDAAMSVWPTKPKYTAGKALYFS 122
 Qy 177 HGFSPPVKDLTKVVEPTDYLVAPKGSGRITVSLFREGRGINNSFAYQDVTGKAKEK 236
 Db 123 HGFAITWSDRGTGVPQDIDVYMAKGSGLSLRTNIFGRGLNSAYIYDVTGKAKEK 182
 Qy 237 AVALGVAVGSGYLWETTPEKEVYSDLYGERCIMGGIHGMFLAQYEVLREGRHSPSEAFN 296
 Db 183 TIALGIGVSGYLWETTPEKEVRLATSDLTGERSLMGAIQGULLAQYEVLRENGHTPSEAFN 242
 Qy 297 ETVEEATOSLYPLIGHGMDDMFDAGCSTTARRGAIDWTPKFDALKPQVFNLYDSYKNGD 356
 Db 243 ETVEEATOSLYPLIGHGMDDMFDAGCSTTARRGAIDWTPKFDALKPQVFNLYDSYKNGD 302
 Qy 357 ERKRSLEYNSQPDYRERYAEELDEIRNLFWRAGK--KRSLRPEN 398
 Db 303 ERQISDSDNSKEDYREKLEAEKALAESEEMQTAIVTRKURPEN 346

Search completed: March 22, 2006, 15:27:06
 Job time : 115.954 secs

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OM protein - protein search, using SW model 1

Run on: March 22, 2006, 15:21:02 ; Search time 113.517 Seconds

(without alignments) 1528.885 Million cell updates/sec

Title: US-10-797-248A-2
Perfect score: 201

Sequence: 1 MLRTQARLICNSRVITAKR.....RNMEIWKGKEVRKLURPENQ (395)

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: _Geneseq_21:*
- 2: _Geneseq_1980s:*
- 3: _Geneseq_2000s:*
- 4: _Geneseq_2001s:*
- 5: _Geneseq_2002s:*
- 6: _Geneseq_2003s:*
- 7: _Geneseq_2003bs:*
- 8: _Geneseq_2004s:*
- 9: _Geneseq_2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2071	100.0	395	6	ABR64304		Abf64304 Acetohydrox acid
2	2071	100.0	395	7	ADK6188		Adk6188 Disease t
3	1667	80.5	400	4	AAU15089		Aau15089 Protein e
4	1667	80.5	400	5	ABP7238		Abp7238 Candida a
5	1508.5	72.8	400	6	ABR64315		Abf64305 Acetohydrox acid
6	1507	72.8	400	6	ABR64306		Abf64306 Acetohydrox acid
7	1507	72.8	400	9	ADV16807		Adv16807 M grisea
8	1503	72.6	402	6	ABR64303		Abf64303 Acetohydrox acid
9	1487.5	71.8	396	6	ABJ26477		Abj26477 Aspergillus
10	1487	71.8	508	6	ABJ26502		Abj26502 Aspergillus
11	1462.5	70.6	388	6	ABJ25902		Abj25902 Aspergillus
12	1462.5	70.6	500	6	ABJ25877		Abj25877 Aspergillus
13	1448.5	69.9	403	9	ADV16810		Adv16810 M graminicola
14	1392.5	67.2	409	7	ADB70124		Adb70124 C. neofor
15	1099.5	53.1	347	6	ABU20976		Abu20976 Protein e
16	495	23.9	332	4	AAB96356		Aab96356 Purative
17	470	22.7	337	6	ABU24174		Abu24174 Protein e
18	465	22.5	331	5	ABB48168		Abb48168 Listeria
19	465	22.5	331	6	ABU32456		Abu32456 Protein e
20	461	22.3	342	4	AAU01250		Aau01250 B. subtilis
21	458.5	22.1	334	4	AAGB1458		Aagb1458 S. epidermidis
22	458	22.1	334	6	ABU42920		Abu42920 Protein e
23	458.5	22.1	339	5	ABP33068		Abp33068 Staphylococcus
24	458.5	22.1	339	8	ADS07053		Ado07053 Staphylococcus

ALIGNMENTS

RESULT 1
ID ABR64304 standard; protein; 395 AA.
XX ABR64304;
XX DT 16-SEP-2003 (first entry)
XX DB Acetohydroxyacid isomero reductase.
XX KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomero reductase; yeast.
XX OS Saccharomyces cerevisiae.
XX PN FR2829363-A1.
XX PD 14-MAR-2003.
XX XX 10-SEP-2001; 2001FR-00011689.
XX PR 10-SEP-2001; 2001FR-00011689.
XX PA (AVET) AVENTIS CROPSCIENCE SA.
XX PI Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
XX DR WPT; 2003-405775/39.
XX PT Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid isomero reductase.
XX PT Claim 2; Fig 1; 66pp; French.
XX PS The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomero reductase. (I) are used for curative or preventive treatment of a wide range of fungal diseases on crops e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomero reductase, used to illustrate the invention
XX SQ Sequence 395 AA;

Query Match 100.0%; Score 2071; DB 6; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.3e-186;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX	PI	Roemer T, Jiang B, Boone C, Bussey H;	OS	Candida albicans.
XX	WPI	2001-489080/53.	XX	WO200253728-A2.
DR		N-PSDB; AAS23417.	XX	PD 11-JUL-2002.
XX	PT	Identifying genes essential to fungal metabolism and identifying potential therapeutic agents that target these genes.	XX	PF 26-DEC-2001; 2001WO-US049486.
XX	PT	targets for therapeutic agents, for creating a collection of identified essential genes, and screening assays for the discovery of new drugs. The invention provides the GRACE (Gene replacement and conditional expression) method for the construction of mutant organisms referred to as GRACE strains of the organism. The invention can be applied to any organism, particularly a pathogenic fungus e.g. Candida albicans, Aspergillus fumigatus and Cryptococcus neoformans. The methods are useful to identify agents that may be used in the treatment of fungal infections. AAU15053-AAU15113 represent proteins encoded by C. albicans essential genes	XX	XX 29-DEC-2000; 2000US-0259128P. PR 20-FEB-2001; 2001US-00791224. PR 22-AUG-2001; 2001US-0314050P.
XX	PS	Claim 43; Page 222-223; 324pp; English.	XX	XX (ELIT-) ELITRA PHARM INC.
CC	CC	The present invention relates to novel methods for constructing fungal strains useful for identification and validation of gene products as targets for therapeutic agents, for creating a collection of identified essential genes, and screening assays for the discovery of new drugs. The invention provides the GRACE (Gene replacement and conditional expression) method for the construction of mutant organisms referred to as GRACE strains of the organism. The invention can be applied to any organism, particularly a pathogenic fungus e.g. Candida albicans, Aspergillus fumigatus and Cryptococcus neoformans. The methods are useful to identify agents that may be used in the treatment of fungal infections. AAU15053-AAU15113 represent proteins encoded by C. albicans essential genes	XX	PA 2002-566694/60. DR N-PSDB; AB231788.
XX	CC	Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.	XX	XX Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
XX	SQ	Sequence 400 AA;	PS	Claim 44; SEQ ID NO 7075; 167pp + Sequence Listing; English.
XX	Query	Sequence 1667; DB 4; Length 400; Best Local Similarity 79.1%; Pred. No. 2.2e-148; Matches 315; Conservative 42; Mismatches 35; Indels 6; Gaps 3;	XX	The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biogenetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential Candida albicans protein used in the method of the invention.
Qy	3	RTOAARL--ICNSRVITAKTFAL--ATRAAAYSRAAERVKPMEITTRGKQINFGGTV 57	CC	CC Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
Db	4	RTTSRMRARIATAKATLSKTFSLANATRYTAASSAAKAMTPITSIRAVKTINFGGTV 63	XX	XX Sequence 400 AA;
Qy	58	ETVYERADWPREKULDXFKNDTFALIJKGGSGQGGLNFLRDNGANVIIIGRKDGASWKA 117	CC	Query Match 80.5%; Score 1667; DB 5; Length 400;
Db	64	EVVHERADWPKERLJLDFKNDTFALIJKGGSGQGGLNFLRDNGANVIIIGRK-GSSWEA 122	CC	Best Local Similarity 79.1%; Pred. No. 2.2e-148;
Qy	118	IEDGWPGKQHFTDAIKGSYVWNLLSSAAQESTWPAKPLITPKGKTLFSHGFSPV 177	CC	Matches 315; Conservative 42; Mismatches 35; Indels 6; Gaps 3;
Db	123	VEDGWPGKGENLFVDEAISGTIMDLSSAAQESTWFWKLPOLTEGKTLFYSHGFSPV 182	CC	3 RTQAARL--ICNSRVITAKTFAL--ATRAAAYSRAAERVKPMEITTRGKQINFGGTV 57
Qy	178	KDLTHVEPPKDLDTVLAAPKGSGRTVRSLEPKERGINSSTAVNDVTGKHEKAOALAYA 237	CC	4 RTTSMEMARLATAKATLSKTFSLIANNATTRYTAASSAAKMTPTISIRGVKTINFGGTV 63
Db	183	KDLTHVEPPNIDVLAAPKGSGRTVRSLEPKERGINSSTAVNDVTGKBEKAALATA 242	CC	58 ETVYERADWPREKULDXFKNDTFALIJKGGSGQGGLNFLRDNGANVIIIGRK-GSSWEA 117
Qy	238	IGSGTYVQTFERETNSD1GERGCLMGHIGMFLAQYDVTRENCHSPSPAFNETVEAT 297	CC	64 EVVHERADWPKERLJLDFKNDTFALIJKGGSGQGGLNFLRDNGANVIIIGRK-GSSWEA 122
Db	243	IGSGTYVQTFERETNSD1GERGCLMGHIGMFLAQYETRENCHSPSPAFNETVEAT 302	CC	118 IEDGWPGKQHFTDAIKGSYVWNLLSSAAQESTWPAKPLITPKGKTLFSHGFSPV 177
Qy	298	QSLVPLIGKGMDDMYDACESTTARGALDVTIPFKNALKVFDQIYESTNGTETKRSLE 357	XX	123 VEDGWPGKGENLFVDEAISGTIMDLSSAAQESTWFWKLPOLTEGKTLFYSHGFSPV 182
Db	303	QSLVPLIGKGMDDMYDACESTTARGALDVTIPFKNALKVFDQIYESTNGTETKRSLE 362	CC	178 KDLTHVEPPKDLDTVLAAPKGSGRTVRSLEPKERGINSSTAVNDVTGKHEKAOALAYA 237
Qy	358	FNSQDYPREKLEKELDTIRNMEIWRVGKEYVRKLRPENQ 395	CC	183 KDLTHVEPPSNIDVIAAPKGSGRTVRSLEPKERGINSSTAVNDVTGKHEKAOALAYA 242
Db	363	FNSRSDYKERLEELQTIIRNMEIWRVGKEYVRKLRPENQ 400	XX	RESULT 4
XX	XX	XX ABP73238	XX	XX ABP73238 standard; protein; 400 AA.
XX	XX	XX ABP73238;	XX	XX ABP73238;
DT	30-JAN-2003	(first entry)	XX	XX Candida albicans essential protein SEQ ID NO 7075.
DE			XX	KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW			XX	KW signal transduction; DNA replication; cell division; growth;
KW			XX	KW proliferation; Candida albicans; fungicide; antifungal.

125 GWPGRNLFEDEAISRGTVMNLLDAQSETNPALKPQITKSKTLYSHGFSPPVFKDL 184
 Db 181 THVEPKDLDVLYVAPKGSSERTVRLPKERGINSISYAWNNDTGKAHKKAQALAVAGS 240
 Qy 185 TKVEPTDVDTLCPKGSGRTVSLFRERGINSFAYQDVTEAEKAIAQVAGS 244
 Db 241 GYVOTTFERVNSDLYGERGCLMGGMFLAQYDVFLERENGHSPEAFTNEYVEATOSL 300
 Qy 245 GYLYKTFERGVSDLYGERGCLMGGMFLAQYDVFLERENGHSPEAFTNEYVEATOSL 304
 Db 301 YPLIGKYGMDYDACSTARRGALDWYIFKNAKLPVFDLYESTKNGTETKRSLEEN 360
 Qy 305 YPLIGANGMDYACSTARRGALDWSPREFKDALKPVNQLYDVSQDSETORSLDYNS 364
 Qy 361 QPDYREKYLEDITRNMIEIWKVGEVRKURPENQ 395
 Db 365 QPDYREKYEAEIMEIIRNLLEIWRAGKAVRSRPPENQ 399

RESULT 7
 ADV16807 standard; protein; 400 AA.
 ID ADV16807
 XX AC ADV16807;
 XX DT 24-FEB-2005 (first entry)
 XX DE M grisea ketol-acid reductoisomerase IIv5 seqid 6.
 XX substrate inhibition; antibiotic; gene disruption;
 XX ketol-acid reductoisomerase; IIv5; enzyme.
 XX OS Magnaporthe grisea.
 XX PN WO2004104176-A2.
 XX PD 02-DEC-2004.
 XX PF 17-MAY-2004; 2004WO-US015404.
 XX PR 15-MAY-2003; 2003US-0470947P.
 XX PR 19-MAY-2003; 2003US-0471615P.
 XX PR 21-MAY-2003; 2003US-0472242P.
 XX (PARA-) PARADIGM GENETICS INC.
 XX PI Tanzer MM, Hamer L, Adachi K, Dezaan TM, Lo SC;
 XX PI Montenegro-Chamorro MV, Daveaux BA, Frank SA, Heininger RW;
 XX PI Mantahty SK, Pan H, Covington AS, Tarpey R, Shuster JR;
 XX DR; 2005-021202/02.
 XX DR-N-PSDB; ADV16805, ADV16806.
 XX PSQ ID NO 6; 179pp; English.
 XX
 XX Identifying a test compound as a candidate for an antibiotic comprises
 PT contacting ornithine carbamoyltransferase (Octase) or keto-acid
 PT reductoisomerase polypeptide, or fungal pathogenicity-confering gene
 PT with a test compound.
 XX
 XX Claim 4B; SEQ ID NO 6; 179pp; English.
 XX
 XX The invention describes a method of identifying a test compound as a
 CC candidate for an antibiotic comprising contacting ornithine
 CC carbamoyltransferase (Octase) or keto-acid reductoisomerase polypeptide,
 CC or fungal pathogenicity-confering gene with a test compound. The method
 CC comprises: contacting Octase polypeptide, keto-acid reductoisomerase
 CC polypeptide, or fungal pathogenicity-confering gene with a test compound
 CC ; and detecting the presence or absence of binding between the test
 CC compound and the polypeptide or gene, where binding indicates that the
 CC test compound is a candidate for an antibiotic. Also described are: an
 CC isolated nucleic acid comprising a nucleotide sequence encoding a
 CC polypeptide having at least 50% sequence identity to, or having at least
 CC 10% of the activity of, 400, 403 or 469 amino acids; and an isolated

CC polypeptide consisting essentially of the amino acid sequence of 400, 403
 CC or 469 amino acids. The methods are useful for identifying inhibitors of
 CC ornithine carbamoyltransferase, keto-acid reductoisomerase, and fungal
 CC pathogenicity-confering gene as antibiotics. This is the amino acid
 CC sequence of Magnaporthe grisea keto-acid reductoisomerase IIv5.
 XX
 Sequence 400 AA;

Query Match 72.8%; Score 1507; DB 9; Length 400;
 Best Local Similarity 73.2%; Pred. No. 2.e-113;
 Matches 289; Conservative 44; Mismatches 56; Indels 6; Gaps 3;

Qy 2 LRTQARLICNSRTVAKRTFALATRAYSRAARFVYP-MITRGKJQINPGGTVERV 60
 Db 10 LRPMPQL --ATPAVQRTFVAASMSYTRAKAA--VAPTQQQIRGKTTMDPAGHKEQV 64
 Qy 61 YERADWPREKLLDYFKNDTFALIGYGSQOGGLNLRDNGLAVNTIGVRKDGAWSKAATED 120
 Db 65 WERADWPREKLLFYFDDTLALIGYGSQOGGLNLRDNGLAVNTIGVRKDGAWSRDAVQD 124
 Qy 121 GMYPGKQULFTVEDAIKRGSSYVMNLLSDAQSETWPAIKPLLPKGKTLYFSSHGFSPPVFKDL 180
 Db 125 GMYEGKQNLFEDEAISRGTVMNLLDAQSETWPAIKPLLPKGKTLYFSSHGFSPPVFKDL 184
 Qy 181 THVEPKDLDVLYVAPKGSSGRVSLFKEGRGINSYAVWNDVTGKAHEKAQLAVALGS 240
 Db 185 TKVEPTDVDTLCPKGSGRTVSLFREGRGINSSFAVYQDVTGEAEKAIALGVALGS 244
 Qy 241 GRYVQTTFEREYNSDLYGERGCLMGGMFLAQYDVFLERENGHSPEAFTNEYVEATOSL 300
 Db 245 GYLKTTFKEVYSDLYGERGCLMGGMFLAQYEVLERGHSPEAFTNEYVEATOSL 304
 Qy 301 YPLIGKYGMDYMDACSTARRGALDWYPIFKNAKLPVFDLYESTKNGTETKRSLEFNS 360
 Db 305 YPLIGANGMDYMEACSTARRGALDWSPRFKDALKPVNQLYDSVKDGSSETORSLDYNS 364
 Qy 361 QPDYREKULEKELDTIIRNBIWKVGEVRKURPENQ 395
 Db 365 QPDYREKYEAEIMEBIRNLLEIWRAGKAVRSRPPENQ 399

RESULT 8
 ABR64303 standard; protein; 402 AA.
 ID ABR64303
 XX AC ABR64303;
 XX AC ABR64303;
 XX DT 16-SEP-2003 (first entry)
 XX DE Acetohydroxyacid isomeroeductase #1.
 XX XX Enzyme; anti-fungal; fungal disease; acetohydroxyacid isomeroeductase.
 XX OS Magnaporthe grisea.
 XX FR2829363-A1.
 XX PD 14-MAR-2003.
 XX PR 10-SEP-2001; 2001FR-00011689.
 XX PR 10-SEP-2001; 2001FR-00011689.
 XX (AVETIS) AVETIS CROPSCIENCE SA.
 XX XX Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
 XX DR WPI; 2003-40575/39.
 XX Treatment of crops, useful for controlling fungi on, e.g. cereals,
 PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
 PT isomeroeductase.

PS Claim 2; Fig 1; 66pp; French.

XX The present invention relates to a method for controlling fungal disease
 CC in crops by applying an inhibitor (II) of acetohydroxyacid
 CC isomerase. (II) are used for curative or preventive treatment of
 CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
 CC rape. The present sequence is an acetohydroxyacid isomerase, used
 CC to illustrate the invention
 XX

SQ Sequence 402 AA;

```
Query Match 72.6%; Score 1503; DB 6; Length 402;
Best Local Similarity 72.9%; Pred. No 7_1e-13;;
Matches 248; Conservative 45; Mismatches 56; Indels 6; Gaps 3;
Qy 2 LRTQARLICNSRVTAKTRAAYSRPARFVTP-MITTRGKQINFGGTIVETV 60
Db 10 LRPMARQL--ATPAVQRSSFAASSMYATRKA--VAPTOQOIQRGVMTDPAHHKEQV 64
Qy 61 YERADWPRLKFLDFFKNDTFAKIGYSGOGYQGOGLNRDNGLAVTIGVRDGASWKAALD 120
Db 65 WERADWPRLKFLDFFKNDTFAKIGYSGOGYQGOGLNRDNGLAVTIGVRDGASWKAALD 124
Qy 121 GWPCKNLITFVEDAIKRGSYVMNLLSDAQSSETWPAIKPLLTIGKTYLPSHGFSVPFKDL 180
Db 125 GWPCKNLITFVEDAIKRGSYVMNLLSDAQSSETWPAIKPLLTIGKTYLPSHGFSVPFKDL 184
Qy 181 TIVEPDKDQDVILVAPKGSGRTVRSLFKRGINSSTAVWNDTGRAHKQAQLAVAGS 240
Db 185 TKVEVPTDDVVLCAPKGSQRTVRSLFKRGINSSTAVWNDTGRAHKQAQLAVAGS 244
Qy 241 GYYQTTFREVNSDLYGERGLCMLGGTMFLAQDYVIRENGHSPSEAFNETVTEATQSL 300
Db 245 GYLTKTFFREVNSDLYGERGLCMLGGTMFLAQDYVIRENGHSPSEAFNETVTEATQSL 304
Qy 301 YPLIGKYGHDYMDACSTARRGALDWYPIKNAKLPYQDLYESTKNGTETRSLEFNS 360
Db 305 YPLIGANGNDWYMEACSTARRGALDWYPIKNAKLPYQDLYESTKNGTETRSLEFNS 364
Qy 361 QPDYREKCEKELDTIRNMEIWKVKEVKKLRPENQ 395
Db 365 QPDYREKTEAEMEBIRNLIWRAKGAVSRSLRPENQ 399
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PS Sequence 402 AA;

XX The invention relates to novel purified or isolated nucleic acids of
 CC essential genes of *Aspergillus fumigatus*. The isolated nucleic acids of
 CC the invention are used to treat or prevent infections by a pathogenic
 CC organism such as *A. fumigatus*, to treat a non-infectious disease in a
 CC subject (e.g. cancer), to prevent or contain contamination of an object
 CC by *A. fumigatus*, or to prevent or inhibit formation on a surface of a
 CC polymeric comprising *A. fumigatus*. The polynucleotides are useful for
 CC expressing recombinant protein for characterisation, screening or
 CC therapeutic use, as markers for host tissues in which the pathogenic
 CC organisms invade or reside, for comparing with the DNA sequence of *A.*
 CC *fumigatus* to identify duplicated genes or paralogues having the same or
 CC similar biochemical activity and/or function, for comparing with DNA
 CC sequences of other related or distant pathogenic organisms to identify
 CC potential orthologous essential or virulence genes, for selecting and
 CC making oligomers for attachment to a nucleic acid array for examination
 CC of expression patterns, for raising anti-protein antibodies, is an
 CC antigen to raise anti-DNA antibodies or to elicit an immune
 CC response, and for identifying poly nucleotides encoding the other protein
 CC with which binding occurs or to identify inhibitors of the binding
 CC interaction. The polypeptides may be used to raise antibodies or to
 CC elicit immune response, as a reagent in assays designed to quantitatively
 CC determine levels of the protein in biological fluids, as a marker for
 CC host tissues in which pathogenic organism invade or reside, and to
 CC isolate correlative receptors or ligands in the case of virulence
 CC factors. This sequence represents a protein of one of the essential genes
 CC of *Aspergillus fumigatus* of the invention
 XX

SQ Sequence 396 AA;

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Query Match 71.8%; Score 1487.5; DB 6; Length 396;
Best Local Similarity 71.6%; Pred. No. 2e-131;;
Matches 280; Conservative 46; Mismatches 62; Indels 3; Gaps 1;
Qy 5 QAARLICNSRVTAKTRFALATRAAAYSRPARFVPMITRGLKQINFGSTVETVYERA 64
Db 8 RAIRL--ARYAAPRTVSAALPRPLAKAAATRAVAASTAPTRGVKTAFADSKEETYERA 64
Qy 65 DMPREKLLDYFNDTFLALIGQSGQGQNLRDNGLAVTIGVRDGASWKAALDQWVP 124
Db 65 DMPREKLLDYFNDTFLALIGQSGQGQNLRDQGQNLVIVGVRDGASWKAALDQWIP 124
Qy 125 GRNLFTVEDAIKRGSYVMNLLSDAQSSETWPAIKPLLTGKTYLPSHGFSVPFKDLTH 184
Db 125 GRNLFTVEDAIKRGSYVMNLLSDAQSSETWPAIKPLLTGKTYLPSHGFSVPFKDLTH 184
Qy 185 PPKDLDVILVAPKGSGRTVRSLFKEGRGINSYYAVNDVYTKAHEKAQALAVAGSGYVY 244
Db 185 VPKDLDVILVAPKGSGRTVRSLFKEGRGINSYYAVNDVYTKAHEKAQALAVAGSGYVY 244
Qy 245 QTTFERVNSDLYGERGLCMLGGTMFLAQDYVIRENGHSPSEAFNETVTEATQSL 304
Db 245 BTTFEREVSDLYGERGLCMLGGTMFLAQDYVIRENGHSPSEAFNETVTEATQSL 304
Qy 305 GRXGMDMYDASTTARRGALDWYPIKNAKLPYQDLYESTKNGTETRSLEFNSQDY 364
Db 305 GANGMDMYAACSTTARRGALDWYPIKNAKLPYQDLYESTKNGTETRSLEVNSQDY 364
Qy 365 REKLEKELDTIRNMEIWKVGEVKKLRPENQ 395
Db 365 REKLEKELDTIRNMEIWKVGEVKKLRPENQ 395
PA (ELIT-) ELITRA PHARM INC.
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expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polymucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which the pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention

Sequence 388 AA;

Query	Match	70.6%;	Score 1462.5;	DB 6;	Length 388;
	Best Local Similarity	71.6%;	Pred. No. 4.4e-128;		
Matches	275;	Conservative	46;	Mismatches	60;
				Indels	3;
				Gaps	1;
Qy	5	QAARLICNRVITAKRITPALETAAYAASRPAARFVKPMITTRGLQINFGGTETVYERA	64		
Db	8	RALRL--ARRAAPRTVISAALPRPAAKATRAAVASTAPVRCKTIAFADSKEVYERA	64		
Qy	65	DWPRPEKLUJYFKNDFTAIIGYGSQCGYQGLNLRDNGIANYIIGYRKDGASWKAIEQDW	124		
Db	65	DWPRBKLUQYFKNDFTAIIGYGSQCGYQGLNLRDQDGW	124		
Qy	125	GKNLFTVEDAIKRGSYVNNLSDAQOSSTWPALKPLTIGKTYFSGFSPVFKLTH	184		
Db	125	GKNLFDLTLTEAVQKGTVINMNLSDAQOSSTWPALKPLTIGKTYFSGFSPVFKLKV	184		
Qy	185	PPKDLDVIVLAVPKGSRGRTRVSLFREGINNSYAWNDVTGKHERAQALAYAAGSSYV	244		
Db	185	VPKDGDVIVLAVPKGSRGRTRVSLFREGINNSYAWNDVTGKHERAQALAYAAGSSYV	244		
Qy	245	QTFEREYNSDLYGERGCLMGTHGMFLAQYDYLRENSHSPSEAFNETVTEATQSLYPL	304		
Db	245	ETTFKEKEYSDLYGERGCLMGTHGMFLAQYDYLRENSHSPSEAFNETVTEATQSLYPL	304		
Qy	305	GKYGMDMNYDACSTTARRGALDWYPIKNAKPVQDLYESTKNGTBTKRSLEFNSDPY	364		
Db	305	GANGMDMNYAACSTTARRGAIIDNSRFDTLKPIFNELYDSDVRDGTETKRSLEFNSDPY	364		
Qy	365	REKLEKELDTIRANNEIWKVKEVR	388		
Db	365	REKYEKEMODIRLEIWRAGKAVR	388		

XX XX 23-APR-2002; 2002WO-US013142.
 CC XX 23-APR-2001; 2001US-0285697P.
 CC PR 2001US-0287068P.
 CC PR 05-JUN-2001; 2001US-0295800P.
 CC PR 09-JUL-2001; 2001US-0303899P.
 CC PR 31-AUG-2001; 2001US-0316362P.
 XX XX (BLIT-) ELTRA PHARM INC.
 PA PA
 PI Jiang B, Tishkoff D, Zamudio C, Broshkin AM, Hu W, Lemieux SM,
 XX XX WBI; 2003-093124/08.
 XX XX New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
 XX XX Disclosure; Page: 175PP; English.
 XX XX
 CC CC The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention
 XX XX Sequence 500 AA;

Query Match 70.6%; Score 1462.5; DB 6; Length 500;
 Best Local Similarity 71.6%; Pred. No. 6.7e-129; Mismatches 46; Indels 60; Gaps 1;
 Matches 275; Conservative 46; Mismatches 60; Indels 3; Gaps 1;
 Qy 5 QAAARLICNRVITAKRITPALETAAYAASRPAARFVKPMITTRGLQINFGGTETVYERA 64
 Db 120 RALRL--ARRAAPRTVISAALPRPAAKATRAAVASTAPVRCKTIAFADSKEVYERA 64
 Qy 65 DWPRPEKLUJYFKNDFTAIIGYGSQCGYQGLNLRDNGIANYIIGYRKDGASWKAIEQDW 124
 Db 65 DWPRBKLUQYFKNDFTAIIGYGSQCGYQGLNLRDQDGW 124
 Qy 125 GKNLFTVEDAIKRGSYVNNLSDAQOSSTWPALKPLTIGKTYFSGFSPVFKLTH 184
 Db 125 GKNLFDLTLTEAVQKGTVINMNLSDAQOSSTWPALKPLTIGKTYFSGFSPVFKLKV 184
 Qy 185 PPKDLDVIVLAVPKGSRGRTRVSLFREGINNSYAWNDVTGKHERAQALAYAAGSSYV 244
 Db 185 VPKDGDVIVLAVPKGSRGRTRVSLFREGINNSYAWNDVTGKHERAQALAYAAGSSYV 244
 Qy 245 QTFEREYNSDLYGERGCLMGTHGMFLAQYDYLRENSHSPSEAFNETVTEATQSLYPL 304
 Db 245 ETTFKEKEYSDLYGERGCLMGTHGMFLAQYDYLRENSHSPSEAFNETVTEATQSLYPL 304
 Qy 305 GKYGMDMNYDACSTTARRGALDWYPIKNAKPVQDLYESTKNGTBTKRSLEFNSDPY 364
 Db 365 REKLEKELDTIRANNEIWKVKEVR 388
 Qy 365 REKYEKEMODIRLEIWRAGKAVR 388
 Db 365 REKYEKEMODIRLEIWRAGKAVR 388
 RESULT 12
 ABJ25877
 XX DT 16-APR-2003 (first entry)
 XX Aspergillus fumigatus essential gene protein #535.
 DE Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response.
 XX OS Aspergillus fumigatus.
 XX PN WO200206090-A2.
 XX PD 31-OCT-2002.
 357 ETTFBCEVYSDLYGERGCLMGTHGMFLAQYDYLRENSHSPSEAFNETVTEATQSLYPL 416

Qy 305 GRYGMDYMDACSTTARRGALDWYPIFKNALKPKVFDLYESTKNGTETKRSLEFNQSPDY 364
 Db 411 GANGMDWYACSTTARRGALDWSSFKDTLKPPIFNELYDSVRDGTEKRSLEFNQSPDY 476

Qy 365 REKLEKELDTIRNMEIMWKGKEVR 388
 Db 477 REYKEKEMQDIRDLEIWRAGKAVR 500

RESULT 13
 ADV16810
 ID ADV16810 standard; protein; 403 AA.
 XX
 AC ADV16810;
 XX DT 24-FEB-2005 (First entry)
 DE M graminicola ketol-acid reductoisomerase KARI sedid 9.
 XX substrate inhibition; antibiotic; gene disruption;
 XX ketol-acid reductoisomerase; KARI; enzyme.
 KW Mycosphaerella graminicola.
 OS Mycosphaerella graminicola.
 PN WO2004104176-A2.
 XX PD 02-DRC-2004.
 XX PF 17-MAY-2004; 2004WO-US015404.
 PR 15-MAY-2003; 2003US-0470947P.
 PR 19-MAY-2003; 2003US-0471615P.
 PR 21-MAY-2003; 2003US-0472242P.
 XX PA (PARA-) PARADIGM GENETICS INC.
 PI Tanzer MM, Hamer L, Adachi K, Dezaan TM, Lo SC; Heiniger RW;
 PI Montenegro-Chamorro MV, Darveaux BA, Frank SA;
 PI Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;
 XX WPI: 2005-021202/02.
 DR N-PSDB; ADV16802, ADV16808, ADV16809.
 XX PT Identifying a test compound as a candidate for an antibiotic comprises
 PT contacting ornithine carbamoyltransferase (Octase) or ketol-acid
 PT reductoisomerase polypeptide, or fungal pathogenicity-conferring gene
 PT with a test compound.
 PS Claim 50; SEQ ID NO 9; 179pp; English.
 XX The invention describes a method of identifying a test compound as a
 CC candidate for an antibiotic comprising contacting ornithine
 CC carbamoyltransferase (Octase) or ketol-acid reductoisomerase polypeptide,
 CC or fungal pathogenicity-conferring gene with a test compound. The method
 CC comprises: contacting Octase polypeptide, ketol-acid reductoisomerase
 CC polypeptide, or fungal pathogenicity-conferring gene with a test compound
 CC ; and detecting the presence or absence of binding between the test
 CC compound and the polypeptide or gene, where binding indicates that the
 CC test compound is a candidate for an antibiotic. Also described are: an
 CC isolated nucleic acid comprising a nucleotide sequence encoding a
 CC polypeptide having at least 50% sequence identity to, or having at least
 CC 10% of the activity of, 400, 403 or 469 amino acids, and an isolated
 CC polypeptide consisting essentially of the amino acid sequence of 400,
 CC or 469 amino acids. The methods are useful for identifying inhibitors of
 CC ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal
 CC pathogenicity-conferring gene as antibiotics. This is the amino acid
 CC sequence of Mycosphaerella graminicola ketol-acid reductoisomerase KARI.
 XX Sequence 403 AA;

Qy 275; Conservative 41; Mis matches 57; Indels 9; Gaps 2;
 Qy 19 KRTFFALATRAAAYSSPAAREVKPKMII-----RGLKQINFGGTVEYRADMREKLL 72
 Db 24 QRSPTAVNA- -SRSPLVPAQKAVTSAFVQVRAKTVDFAGDKVKFVFRDDMREKLL 80

Qy 73 DYFKNDTFLALIGYGSQGCGCLNLRDGLNVIIGVRDKGASWKAJEDGMPGKMLKFTVS 132
 Db 81 BYFKNDTFLALIGYGSQGKGGLNLRDGLNVIIGVRKGASWKALEGDWVGEKGLFID 140

Qy 133 DAIKRGSYWYNNLSSDAQSETWPAKPLJTKGKTLIYFSGHSPVYEDPKDLYTHVEPKPDLYI 192
 Db 141 TAIGGTIIMNLLSSDAQSETWPKI KPMLKTKGKTLIYFSGHSPVYEDPKDQTKVEVPDIDV 200

Qy 193 LVAPPGSGSRTVRSLEKEGRGINSYAWNDVTGKHEKAQALAVAGSGVYVQTTFREV 252
 Db 201 LVAPPGSGSRTVRSLEKEGRGINSYAWNDVTGKHEKAQALAVAGSGVYVQTTFREV 254

Qy 253 NSDLYGERTGGLMGGHGMFLAQYDVLRENGHSPSEAFNETVEEAQSLPLIGKGMGYM 312
 Db 261 YSDLYGERTGGLMGGHGMFLAQYDVLRENGHSPSEAFNETVEEAQSLPLIGKGMGYM 320

Qy 313 YDAGCTTARGALDWYPIFKNALKPKVFDLYESTKNGTETKRSLEFNSQPDYREKLEKL 372
 Db 321 YEAGCTTARGALDWSKRFKETLKPVFDLYESTKNGTETKRSLEFNSQPDYREKLEKL 380

Qy 373 DTIRMEIWKVGKVRKURPEN 394
 Db 381 EERINLEIWKVGKVRKURPEN 402

RESULT 14
 ADB70124 standard; protein; 409 AA.
 XX ADB70124;
 AC ADB70124;
 XX DT 04-DEC-2003 (first entry)
 DE C. neoformans amino acid sequence SEQ ID NO:3168.
 XX KW fungicide; gene therapy; infection.
 OS Cryptococcus neoformans.
 XX PN WO200302076-A2.
 XX PD 26-JUN-2003.
 XX PF 17-DEC-2002; 2002WO-US040225.
 XX PR 17-DEC-2001; 2001US-0341261P.
 XX PA (ELITA-) ELITA PHARM INC.
 XX PI Zamudio C, Broshkin AM;
 XX DR WPI; 2003-533017/50.
 XX N-PSDB; ADB65041.
 XX PT New nucleic acid, useful for preparing a composition for treating an
 PT infection caused by Cryptococcus neoformans.
 XX Claim 9; SEQ ID NO 3168; 136pp; English.
 XX The invention relates to a novel purified or isolated Cryptococcus
 CC neofomans nucleic acid molecule comprising a sequence encoding a
 CC polypeptide comprising a sequence not given in the specification. A
 CC polynucleotide of the invention has fungicide activity, and may have a
 CC use in gene therapy. The nucleic acid is useful for preparing a
 CC composition for treating an infection caused by Cryptococcus neoformans.
 CC The present sequence represents a C. neoformans sequence of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC

